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GenCore version 5.1.6
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Database : Post-processing: Minimum Match 0%
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Listing first 45 summaries Minimum DB Maximum DB Title: Perfect score: OM nucleic - nucleic search, using sw model Searched: Scoring table: Run on: tal number of hits satisfying chosen parameters: seq length: 0 seq length: 2000000000 June 29, 2003, 07:22:59; Search time 1244 Seconds
(without alignments)
13872.961 Million cell updates/sec IDENTITY_NUC Gapop 10.0 , Gapext 1.0 2054640 segs, 14551402878 residues US-10-020-338-8 593 GenEmbl: * cccggtcgacccagcgtccg.....catacaaaaatgtcacaagc 593 gb_ba:* gb_htg:* gb_in:* em_vi: *
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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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REFERENCE AUTHORS		ORGANISM	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	HVU249146
FOOLUGE: ITTLICERE; HOTGEUM. 1 (Dases I to 1203) Schmitz, J., Franzen, R., Ngyuen, T.H., Garcia-Maroto, F., Pozzi, C., Salamini, F. and Rohde, W.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	Hordeum vulgare subsp. vulgare	m8 gene; MADS-box protein 8.	'AJ249146.1 GI:9367312	AJ249146	<pre>c protein 8 (m8 ger</pre>	HVU249146 1203 bp mRNA linear PLN 14-JUL-200	

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Submitted (20-AUG-1999) Softer Zuechtungsforschung,
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  Lolium temulentum MADS-box protein spliced product, complete cds. AF035379
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g, Carl von Linne Weg 10, 50829 Koeln,
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1 (bases 1 to 1062)

Gocal, G.F.W., Blundell, C., Schwartz, O.M.

Expression of Two APETALA1-Related Genes
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Submitted (20-NOV-1997) PBIO, Salk Inst Rd., La Jolla, CA 92037, USA
Location/Qualifiers
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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HAQQNLCYPLVTMGGEAVAAAPGQQGELRIGGLPPWMLSHLNA"
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The maize MADS box gene ZMMADS3 affects node number of development and is co-expressed with ZmMADS1 during development, in egg cells, and early embryogenesis plant Physiol. 127 (1), 33-45 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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Heuer, S., Dresselhaus, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
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TCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTGAA
             TCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAA
                                                   CGACTCCCGCATGGACAAAATTCTAGAACGTTATGAGCGATATTCCTATGCTGAAAAGGC
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uer,S., Dresselhaus,T. and Loerz,H.
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/product="MADS box protein 3"
/protein_id="AAG43200.1"
/protein_id="AAG43200.1"
/bxref="GI:12002141"
/db xref="GI:12002141"
/translation="MGRGKVQLKRIENKINRQVTFSKRRUGLLKKAHEISVLCDAEVA
/IVFSPKGKLYEYASDSRMDKILERYERYSYABEALISAESSSGNWCHEYRKLKAKI
ETIQRCHKHLMGEDLESLNPKELQOLEQGLESSLKHIRSRKSHLMAESISELQKKERS
LØENKILQKELSERQKAVASRQQQQQVQWDQQTQVTSSSSSSFMMRQDQQGLP
PPQNICFPPLSIGERGEEVAAAAQQQLPPPGQAQPQLRIAGLPPWMLSHLNA"
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Pred. No. 4.6e-62;
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Query Match
Best Local Similarity
Matches 316; Conserv
Seed plants exhibiting inducible ea
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Patent: US 6002069-A 7 14-DEC-1999;
Location/Qualifiers
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Yanofsky, M.F.
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Yanofsky, M.F.
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Location/Qualifiers
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Matches 316; Conserv
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Yanofsky, M.F.
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                                                                 TCCTCTGTGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGT
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                      ACGCCACCGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTG
                                                 TCCTCTGCGATGCCGAGGTCGCCGTCATCGTCTTCTCCCCCAAGGGCAAGCTCTACGAGT
 ACGCCACCGACTCCCGCATGGACAAATTCTTGAACGCTATGAGCGATATTCCTATGCTG
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373 c 358 g
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1. .1345
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373 c 358 g
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patent US 6127123
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Pred. No. 1.6e-61;
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Pred. No. 1.6e-61;
0; Mismatches 26;
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RESULT 8
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Best Local Sim
Matches 316;
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1 L46400
1 L46400.1 GI:939784
MADS box protein.
2ea mays cDNA to mRNA.
4 Zea mays cDNA to mRNA.
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Sequence 7
AR200417
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1345)
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373 c 358 g
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Pred. No. 1.6e-
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TITLE
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                               Sorghum bicolor.
Sorghum bicolor
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Trache
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
clade; Panicoideae; Andropogoneae; Sorghum.
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U32110.1
Greco,R.,
Pe,M.E.
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                      (bases 1 to 1186)
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PPPHNICFPPLTMGDRGEELAAAAAAQQQQPLPGQAQPQLRIAGLPPWMLSHLNA"
         Stagi,L.,
                                                                                                                     GI:1905933
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/tissue_type="female inflorescence"
/dev_stage="immature ear"
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         Colombo, L.,
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Pred. No. 1.6e-61;
0; Mismatches 26
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         Angenent, G.C.,
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         Sari-Gorla, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303;
                                                                                                                                                                                                                                                                                                                                                                                        61
Oryza sativa.
Oryza sativa
Coryza sativa
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnollophyta;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                             AF058698.1
                                                                                        Oryza sativa MADS15
AF058698
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97218034
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Genetica e Biologia dei
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                                                                                                                                                                                                                                 AATCTGAAAGTGAGGGAAACTGGTGCCACGAATACAGGAAACTGAAGGCCAAAATTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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SPKKLYEYATDSRMDKILERYERYSYAEKALISAESESGMETESYKKKKKKIEIQE
KCHKHLMGEDLESLNPKELQOLEQQLESSLKHIRSRKSHLMAESISELÇKKKKERSLQEE
NKALQKELAERQKAAASRQQQQGAVGPADTDPGPDKLIIVLHDEAGSAGSAASTKHM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=3
/product="MADS box protein"
/protein_id="AAB50181.1"
/db_xref="GI:1905934"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stagi,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SbMADS2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Sorghum bicolor"
/db_xref="taxon:4558"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="putative
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Pred. No. 1.4
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Microrganismi, Via Celoria 2
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yta; Liliopsida;
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             Embryophyta; Tracheophyta; a; Poales; Poaceae;
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                                                                                                    linear cds.
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99373407
                                                                                                BD012691
A gene co
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Hyoja-dong, Nam-gu, Pohang, Kyungbuk 790-784, Republic
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Moon,Y.H., Kang,H.G., Jung,J.Y., Jeon,J.S., Sung,S.K. and Determination of the motif responsible for interaction be rice APETALAI/AGAMOUS-LIKE9 family proteins using a yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 1285)
Moon, Y.H., Kang, H.G.
Oryza
Oryza
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                                         gene, an microorganism of controling of branch of BD012691
BD012691.1 GI:22092880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                            WO 0114559-A/1.
                                                                                                                                                                                                      GAAACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC 593
                                                                                                                                                                                                                                                                                                     GTACGCCACTGACTCCAGGATGGACAAAATCCTTGAACGTTATGAGCGCTATTCATATGC
                                                                                                                                                                                                                                                                                                                       GTACGCCACCGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGC
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                                                                                                                                                                                                                                                              TGAAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAG
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on,Y.-H., Jang,S.K. and
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sativa.
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AIVESPKGKLYEYATDSRMDKILERYERYSYAEKALISAESESEGNWCHEYKLKAKI
ETIQKCHKHLMGEDHESLNLKELQQLEQQLESSLKHIISRKSHLMLESISELQKKERS
LQEENKALQKELVERQKNVRGQQQVGQWDQTQVQAQAQAQPQAQTSSSSSMLRDQQA
LLPPQNICYPEYMMGERNDAAAAAVAAQGQVQLRIGGLPPWMLSHLNA"
308 c 332 g 272 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="MADS15 protein"
/protein_id="AAF19048.1"
/db_xref="GI:6606072"
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db_xref="taxon:4530"
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89.0%;
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.922
                                                                                                1289 bp
for branching
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                                                                     of plant.
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Pred. No. 2.:
                                                                                1289 bp DNA linear branching of plants, a vector containing said vector and a
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nes 38;
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                                                                                                                                            protein,
AB003325
AB003325
                                         MADS box-like protein.

Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare)
Cryza sativa (japonica cultivar-group) (cultivar:Nipponbare)
panicle at pre-meiotic stage cDNA to mRNA, clone_lib:cDNA panicle
at pre-meiotic stage clone:E31864.
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                      Oryza sativa (japonica
 Shinozuka, Y.,
                               Ehrhartoideae;
```

complete

cds,

1289 bp mRNA 1 cultivar-group) mRNA clone:E31864.

linear F A for MADS

PLN 21-MAR-2002 box-like

GI:5295983

Yamamoto, K. and Oryzeae;

Sasaki,T

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Query Match
Best Local Similarity
Matches 306; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene, an microorganism containing said vector and controling of branch of plant patent: WO 0114559-A 1 01-MAR-2001; KUMIAI CHEMICAL INDUSTRY CO LTD, MINEO KOJIMA, TAKU NOZUE, HIDENARI SHIOIRI OS Oryza sativa (rice) PN WO 0114559-A/1 PD 01-MAR-2001 WO 2000JP005537 PF 18-AUG-2000 WO 2000JP005537 PR 19-AUG-1909 JP 99P 232318 PI 19-AUG-1909 JP 99P 323318 PI MINEO KOJIMA, TAKUJI SASAKI, MASAYUKI NOZUE, HI CI2N15/29, A01H5/00 Location/Qualifiers.
                                                                                                                                                                                                                  430 GTACGCCACCGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGC
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Kojima,M., Sasaki,T., Nozue,M. and Shioiri,H.

Kojima,M., Sasaki,T., Nozue,M. and Shioiri,H.

A gene controling for branching of plants, a vector containing

A gene controling for branching said vector and a method for
                                                                                                                                                                                                                                                                                                                                                         CAGGCAGGTGACGTTCTCCAAGAGGAGGAATGGATTGCTGAAGAAGGCGCACGAGATCTC
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                         GAAACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC
                                                                                                                                                                                                                                                                                               CGTCCTCTGTGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGGTCTATGA
                                                                                      TGAAAAGGCTCTTATTTCAGCTGAATCCGAGAGTGAGGGAAATTGGTGCCATGAATACAG
                                                                                                                                TGAAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAG
                                                                                                                                                                          GTACGCCACTGACTCCAGGATGGACAAAATCCTTGAACGTTATGAGCGCTATTCATATGC
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GAAACTTAAGGCAAAGATTGAGACCATACAAAAATGTCACAAAC
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Location/Qualifiers.
1..1289
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/db_xref="taxon:4530"
_316 c 337 g 28:
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89.0%;
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Pred. No. 2.1e-57;
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RESULT 13
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AUTHORS
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Best Local Sim
Matches 306;
  an microorganism
                             A gene controling
                                                                                       08-FEB-2002
08-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-APR-1997) Takuji Sasaki, National Institut
Agrobiological Resources, Rice Genome Research Program;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                      standard;
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AIVFSSPKGKLYEYATDSRMDKILERYERYSVAEKALISAESESEGNWCHEYRLKAKI
ETIQKCHKHLMGEDLESLNLKELQQLEQOLESSLKHIISRKSHLMLESISELQKKERS
LQEENKALQKELVERQKWURGQQQVQQTQVQAQAQAQPQAQTSSSSSSMLRDQQA
LLPPQNICYPPVMMGERNDAAAAAVAAQGQVQLRIGGLPPWMLSHLNA"
316 c 337 g 282 t
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/product="MADS box-like protein"
/protein_id="BAA81883.1"
/db_xref="GI:5295984"
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E31864"
     containing
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  for branching of plants, a ontaining said vector and a
                                                                                    70,
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                                                                                    Created)
Last updated,
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Pred. No. 2.1e
0; Mismatches
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     vector and a method
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No. 2.1e-57;
                                                                                       Version 1)
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at pre-meiotic stage"
                               vector
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RESULT 14
AF345911
LOCUS
DEFINITION
ACCESSION

AF345911 Oryza sativa AF345911

MADS-box

1347 bp mRNA protein FDRMADS3 (

mRNA,

linear P: A, complete

PLN 02-OCT-2001

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Best Local (
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"A gene controling for branching of plants,
an microorganism containing said vector and
branch of plant",
Patent number JP03075374-T/1, 16-FEB-2001.
KUMIAI CHEMICAL INDUSTRY CO LTD, MINEO KOJIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Snermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhart
                                                                                                                                                                                                                                                                                                      Sequence 1289 BP; 354 A; 316 C; 337 G; 282 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             source
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Oryzeae; Oryza.
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C12N15/29, A01H5/00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (rice)
JP 03075374-T/1
                                                                                                                                                                                                                                                                                                                                                                                                      source
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19-AUG-1999 JP 99P 232318
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                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                               GCGAAATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAA
            GAAACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC
                                                                                   GTACGCCACTGACTCCAGGATGGACAAAATCCTTGAACGTTATGAGCGCTATTCATATGC
                                                                                                       GTACGCCACCGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGC
                                                                                                                                                                                    TCGGCAGGTGACCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTC
                                                            TGAAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAG
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                                        TGAAAAGGCTCTTATTTCAGCTGAATCCGAGAGTGAGGGAAATTGGTGCCATGAATACAG
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/organism="Oryza sativa"
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89.0%;
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                                                                                                                                                                                                                                                                        Score 283.2;
Pred. No. 2.1
                                                                                                                                                                                                                                                              Mismatches
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AB007504
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Best Local Similarity
Matches 305; Conserv
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AB007504
AB007504.1 GI:3688588
TAWADS#11; MADS box transcription factor.
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1 (bases 1 to 1347)
                        Triticum aestivum young spike cDNA to mkwa.
Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Macmoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                     AB007504
Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (06-FEB-2001) Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gao, Z., Chen, R., Jia, H. and Sun, C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
Murai,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCGAAATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAA
                                                                                                                                                                                                                                         GAAGCTTAAGGCAAAGATTGAGACCATACAAAAATGTCACAAAC 455
                                                                                                                                                                                                                                                           GAAACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MGRGKVQLKRIENSMNRQVTFSKRRNGLLKKAHEISVLCDAEVA
AIVESPKGKLYEYATUSRMDKILERYERYSYARKALISAESESEKGNWCHEYKLKAKI
ETIQKCHKHLMGEDLESLULKELQQLEQQLESSLKHIRSRKSHLMLESISELQKKERS
LQEENKALQKELVERGKUVRGQQQVGGWDQTQVQAQAQAQPQAQTSFFFFMLRDQQA
LLSPQNICYPFVMMGQRNDAAARRWRPKARCNFRIGGFPPMMLSTFKA"
1313 c 354 g 304 t
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/product="MADS-box_protein_FDRMADS3"
/protein_id="AAL09473.1"
/db_xref="GI:15824795"
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ocation/Qualifiers
Murai,R.,
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'db_xref="taxon:4530"
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and Ogihara, Y
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or MADS box transcription factor,
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259 GGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murai,K., Takumi,S., Koga,H. and Ogihara,Y. Pistilody, homeotic transformation of stamens into structures, caused by nuclear-cytoplasm interaction plant J. 29 (2), 169-181 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murai,K., Murai,R., Takumi,S. and Ogihara,Y. cDNA cloning of three MADS box genes in wheat AB007504, AB007505 and AB007506) (PGR98-159) Plant Physiol. 118, 330 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University Extension Press,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                             GACCTTCTCCAAGCGCCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTG
                                                                                                                                                                                                                                                                                                                                                     GGAGATGGGGCGCGGGAAGGTGCAGCTGAAGCGGATCGAGAACAAGATCAACCGGCAGGT
                                                                                                                                                                                                                                                GACCTTCTCCAAGCGCCGCTCGGGGCTGCTCAAGAAGGCGCACGAGATCTCCGTGCTCTG
TCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAA
                                                                                                                                                 CGACGCCGAGGTCGGCCTCATCATCTTCTCCACCAAGGGAAAGCTCTACGAGTTCTCCAC
                                                                                                                                                                                               TGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCAC
                                                                                               CGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAAGGC 498
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/db_xref="taxon:4565"
/tissue_type="young spike"
l. .1161
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/protein_id="BAA33457.1"
/db_xref="GI:3688589"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="20 a nucleotides"
282 c 301 g 270
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0; Mismatches 44
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Search completed: June 29, 2003, 07:50:49 Job time: 1247 secs

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Maximum
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Kesult	1	Query					
No.	Score	Match Length DB	Length	DB	ij	Description	
1	302.6	51.0	496	21	AAC43733	Zea mays DNA fragm	
N	302.6	51.0	1250	22	AAF85192	Nucleotide sequenc	
ω	300.4	50.7	1342	18	AAT99437	Maize floral meris	
4	300.4	50.7	1345	19	AAV58307	Zea mays AP1 gene.	
ហ	300.4	50.7	1345	19	AAT86631	APETALA1 gene from	
თ	300.4	50.7	1345	19	AAV02763	Maize floral meris	
7	300.4	50.7	1345	19	AAV06021 ·	Maize floral meris	
8	300.4	50.7	1345	21	AAC61410	cDNA encoding a AP	
9	300.4	50.7	1345	21	AAZ57057	Zea mays ZAPI prot	

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AAV02762	AAT86630	AAV58317	AAT76887	AAC41877	AAV99856	AAX18594	AAZ92142	AAZ57055	AAC61408	AAV06019	AAV02761	AAT86629	AAV58316	AAT76886	AAZ49161	AAA15016	AAC61407	AAV58306	AAT76885	AAC37677	AAC51102	AAZ92141	AAZ57054	AAV06018	AAV02760	an.	AAC90635	AAC55901		AAC44058		443	4105	F7574	AAZ92144
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ALIGNMENTS

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ID AAC43733;
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21-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 30-APR-1999; 30-APR-1999; 06-MAY-1999; 06-MAY-1999; 11-MAY-1999; 11-JUN-1999; 11-JU	19-APR-1999;
99US-0130510 99US-0130510 99US-0130510 99US-0132048 99US-0132484 99US-0132486 99US-0132486 99US-0134218 99US-0134218 99US-0134218 99US-0134218 99US-0134218 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-0134219 99US-0136392 99US-0136782 99US-0137528 99US-0137528 99US-0137528 99US-0139454 99US-0139454 99US-0139454 99US-0139458 99US-0139459 99US-0139461 99US-0139462 99US-0139459 99US-0139462 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-0139463 99US-01439463 99US-0142803 99US-0142803 99US-0142803 99US-0144086 99US-0144332 99US-0144333	US-013
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14-OCT-1999;
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                                                                                                                                                ZmMADS3; flower development; flower structure;
development; transgenic plant; ss.
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RESULT 3
AAT99437
ID AAT9
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Maize floral

11-MAY-1998 AAT99437; AAT99437

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standard;

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185 378 125

245

318

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Floral meristem identity gene; APETALA1; AP1

gene; maize; ZAP-1;

meristem identity gene APETALA (AP1 or ZAP-1) cDNA

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Matches 314;
                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a maize MAD3 protein, designated ZmMADS3. The ZmMAD3 protein is essential for flower development and is active in flowers, in particular, in immature flowers and female flowers, but also in the mature embryo sac of maize. The ZmMAD3 protein is also active in nodes and adjacent cell layers. ZmMAD3 polynucleotides and polypeptides are useful influencing flower structure, function and seed or fruit development in transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide encoding ZmMADS3 protein, for use in cloning expression in plant a nucleic acid sequence encoding protein influencing flower structure, function and/or its seed and/or fr
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1250 BP; 361 A; 295 C; 352 G; 242 T; 0 other;
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P-PSDB; AAB68357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
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               GGCGAAGATTGAGACCATACAAAAATGTCACAAGC
                                                       TCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTGAA
                                                                      TCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAA
                                                                                                               CGACTCCCGCATGGACAAAATTCTAGAACGTTATGAGCGATATTCCTATGCTGAAAAGGC
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GGCCAAAATTGAGACCATACAAAGATGCCACAAGC
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C conversion of shoot meristem to floral meristem. The clone was conversion of shoot meristem to floral meristem. The clone was conversion of shoot meristem to floral meristem. The clone was conversion as Zea mays ear cDNA library using Arabidopsis API C cDNA (see AAT76885) as probe. Sequence homology indicates that C cDNA (see AAT76885) as probe. Sequence homology indicates that converted to floral meristem to a few basal to flowers by inflorescence shoots that are not subtended by flowers. When API is ecotopically expressed in shoot meristem, the shoot meristem is converted to floral meristem and early flowering can occur. The invention relates to floral meristem identity genes API, LFY and especially CAI (see AAT76885-97 and AT99437) and their use in converting shoot meristem to floral meristem and in promoting early flowering in transgenic plants, especially angiosperms such as cereal plants, leguminous plants, oilseed plants, trees, fruit-bearing plants and ornamental flowers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1345 BP; 349 A; 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes the Zea mays AP1 protein (ZAP1). This sequence was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER (CAL) protein of the invention. An expression vector containing the CAL DNA sequence can be used to convert shoot meristems to floral meristems.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             especially to promote early flowering in angiosperms.
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P-PSDB; AAW69328.
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                                                                                                                                                                       The present sequence encodes a floral meristem identity gene product, CC APETALAI (API), from Zea mays. The invention relates to a non-naturally occurring seed plant comprising a first ectopically expressible nucleic acid encoding a first floral meristem identity gene product, provided that the first nucleic acid is not ectopically expressed due to a mutation in an endogenous TERMINAL FLOWER gene. The invention describes of converting shoot meristem to floral meristem, especially in order to promote early reproductive development, in an angiosperm, which comprises introducing a first ectopically expressible nucleic acid molecule encoding a first floral meristem identity gene product into the angiosperm. Ectopic expression of the floral meristem gene product in the shoot meristem tissue of the transgenic plant, allows selection of the time of seed development in the plant which can be useful for manipulating the time of crop harvest in seed-derived crops such as grapes, beans, corn, wheat, rice, hop, etc., or to hasten the breeding of e.g. tree species, for insect or disease resistance.
   Query Match
Best Local Similarity
Matches 316; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic plant comprising an ectopically expressed floral meristem gene - for promoting early reproductive development and controlling the time of seed-derived crop harvest(s) in e.g. grapes, beans,
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P-PSDB; AAW43112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic plant; ectopically AP1; CAULIFLOWER; CAL; LEAFY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APETALA1 gene from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT86631 standard;
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                                                                                                                           1345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yanofsky
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                                                                                                                     349 A; 373 C; 358 G;
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Score 300.4; DB 1
Pred. No. 3.3e-75;
0; Mismatches 26
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LFY; reproductive development;
                                                                                                                        265 T; 0 other;
                                                            DB 19;
                                                            Length
                                                            1345;
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Conservative

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Gaps

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This sequence comprises maize APETALA (ZAP1) cDNA, which encodes a floral meristem identity gene product (see AAW39134) that is involved in the conversion of shoot meristem to floral meristem. It was isolated from an immature ear cDNA library using Arabidopsis AP1 cDNA (see AAV02760) as probe, and is suggested the maize orthologue of AP1. Mutation of the AP1 gene results in replacement of basal flowers by inflorescence shoots that are no

are not in

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RESULT 6
AAVOZ763
ID AAVO
XX AAVO
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                                                                                                                                                                                                                                                   e.g.
                                                                                                                                                                                                                                                                        Nucleic acids encoding AP1 floral meristem identity gene product from cauliflower and maize - useful for promoting early reproductive development and controlling the time of seed-derived crop harvest in
                                                                                                                                                                                                      Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-041770/04.
P-PSDB; AAW39134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floral meristem identity gene; APETALA1; AP1; ZAP1; transgenic plant; angiosperm; seed development; mai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maize floral
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                                                                                                                                                                                                 Page 125-127; 156pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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P-PSDB; WPI;

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AAW43329

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RESULT 7
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Best Local S
Matches 316
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                                                                                                  04-JUN-1997;
                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                            Floral meristem identity gene; transgenic plant; angiosperm; s
                                                                                                                                                                                                                                                                                                                         Maize floral meristem identity
                                                                                                                                                                                                                                                                                                                                                         08-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                    AAV06021;
                                                                                                                                                                                                                                                                                                                                                                                                                AAV06021 standard; cDNA; 1345 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1345 BP;
             Yanofsky MF
                                                                     05-JUN-1996;
                                                                                                                               11-DEC-1997.
                                                                                                                                                            WO9746079-A1
                                                                                                                                                                                                                                                   Zea mays.
                                         (REGC ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 GAAATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGATAGAGAAGAACAAGATAAATC
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                                          CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                       (first entry
                                                                     96US-0659188
                                                                                                  97WO-US09682
                                                                                                                                                                                                       Location/Qualifiers 149..970
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Pred. No. 3.3e-75;
0; Mismatches 26;
                                                                                                                                                                                                                                                                               APETALA1;
seed develo
                                                                                                                                                                                                                                                                                                                         gene APETALA1 orthologue cDNA
                                                                                                                                                                                                                                                                               development;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265 T; 0 other;
                                                                                                                                                                                                                                                                                             AP1;
                                                                                                                                                                                                                                                                                             ZAP1; maize;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Similarity

50.7%;

.3e-75; DB 19;

Length

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This sequence comprises maize ZAP1 cDNA, which encodes a floral meristem identity gene product (see AAW43329) that is involved in the conversion of shoot meristem to floral meristem. It was isolated from an immature ear cDNA library using Arabidopsis AP1 cDNA (see AAV06018) as probe, and is suggested to be the maize orthologue of AP1. Mutation of the AP1 gene results in replacement of basal flowers by inflorescence shoots that are not subtended by flowers. The invention relates to a recombinant nucleic acid molecule that comprises an inducible regulatory element (see AAV06018-24) operably linked to a nucleic acid molecule (see AAV06018-24) encoding a floral meristem identity gene product (see AAV06018-24) encoding a floral meristem (CAL) or LEAFY (LFY). The nucleic acids are used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of floral meristem identity genes to convert shoot meristem floral meristem - for promoting early reproductive development i the plants and control timing of seed-derived crop harvest(s) in
Sequençe 1345 BP; 349 A; 373 C; 358 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 110-112; 147pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. grapes,
                                        transgenic plants, thereby promoting early reproductive development in these plants. This can be useful for manipulating the time of crop harvest in seed-derived crops and to hasten breeding time.
                                                                                                                convert shoot meristem tissue into floral meristem tissue in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         beans, corn and wheat
265
T; 0 other;
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RESULT 8
AAC61410
ID AAC6
XX
AC AAC6
XX
AC CACC
XC
AC AAC6
XX
AC AC6
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AC6
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AC6
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AC7
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Best Local Simi
Matches 316;
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                                                                                                                          APETALA1;
                                                                                                                                                                                      cDNA encoding a APETALA1 (AP1) polypeptide
                                                                                                                                                                                                                                                            19-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                          AAC61410 standard;
                                                                                                floral
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                                                                                                                          AP1;
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                                                                                                meristem;
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                                                                                                                          floral
                                                                                                                                                                                                                                                                                                                                                                                       CDNA; 1345
                                                                                                                                                                                                                                                            entry)
                                                                                                meristem identity gene;
early flowering; ds.
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Pred. No. 3.3e
0; Mismatches
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                                                                                                                              CAULIFLOWER; CAL; LEAFY;
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RESULT 9
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Best Local S
Matches 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a Brassica having a cauliflower phenotype involves detecting a polymorphism associated with cauliflower locus comprising modified cauliflower allele that does not encode active cauliflower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-618379/59.
P-PSDB; AAB19244.
19-MAY-2000
                          AAZ57057;
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                                                    standard;
                                                                                                                                                                                                                                                                                                                                                   GGCAGGTGACCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCG
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                                                                                                                                                                                                                                                                                               TCCTCTGTGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGT
                                                                                                                                                                                                                                                                                                                                   GGCAGGTGACCTTCTCCAAGCGCCGGAACGGCCTGCTCAAGAAGGCGCACGAGATCTCCG
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                                                                                                                                          AACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC 593
                                                                                                                                                                                             AAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGA
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(first
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                                                    DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.7%;
                                                    1345
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 300.4; | Pred. No. 3.3e
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                                                    ВP
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Best Local S
Matches 316
                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a new non-naturally occurring seed plant that comprises a first ectopically expressible nucleic acid molecule encoding a floral meristem identity gene product, provided that the seed plant does not contain a mutation in an endogenous TERMINAL FLOWER (TFL) gene that results in ectopic expression of CAL. The non-naturally occurring seed plant exhibits early reproductive development. The method of promoting early reproductive development can make breeding of long generation seed plants such as trees practical. The method can be used to increase floral meristem identity gene product expression in different crop fields at different times, resulting in a staggered time of harvest for the different fields. The present sequence represents a Zea mays
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New transgenic seed plant exhibiting early reproductive comprises a CAULIFLOWER encoding nucleic acid and a non-endogenous TERMINAL FLOWER gene -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 5; Columns 59-64; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yanofsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays ZAP1 protein encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US6025543-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reproduction;
                                                                                                                                                                                                                                                                                                                                                                                                                       protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-181843/16.
DB; AAY67553.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant; floral meristem; mutation; TFL
pduction; plant breeding; AP1 protein;
         552
                                        378
                                                                    492
                                                                                                 318
                                                                                                                            432
                                                                                                                                                                                     372
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                                                                                                                                                                                                                                              312
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                                                                                                                                                                                                                                                                                                       252
                                                                                                                                                                                                                                                                                                                                    316;
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                                                                                                                                                                                                                                                                                                                                                  Similarity
AACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC
                                                         AAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGA
                                                                                                 ACGCCACCGACTCCCGCATGGACAAAATTCTTGAACGCTATGAGCGATATTCCTATGCTG
                                                                                                                ACGCCACCGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTG
                                                                                                                                                                                                                  GGCAGGTGACCTTCTCCAAGCGCCGGAACGGCCTGCTCAAGAAGGCGCACGAGATCTCCG
                                                                                                                                                                                                                                 GGCAGGTGACCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCCG
                                                                                                                                                                                                                                                                          GCAACAAGGCGATGGGGCGCGCGAAGGTACAGCTGAAGCGGATAGAGAACAAGATAAACC
                                                                                                                                                                                                                                                                                                GAAATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATC
                                                                                                                                                                                                                                                                                                                                                                                            1345 BP;
                                                                                                                                                         TCCTCTGCGATGCCGAGGTCGCCGTCATCGTCTTCTCCCCCAAGGGCAAGCTCTACGAGT
                                                                                                                                                                           TCCTCTGTGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGT
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0655241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0655241
                                                                                                                                                                                                                                                                                                                                                                                            349 A; 373
                                                                                                                                                                                                                                                                                                                                               50.7%;
                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                  Score 300.4;
Pred. No. 3.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            265
                                                                                                                                                                                                                                                                                                                                                3e-75;
                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                            <del>.,</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; CAL;
ds.
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                                                                                                                                                                                                                                                                                                                                                                                            other;
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                                                                                                                                                                                                                                                                                                                                                              Length
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 316; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the APETALA1 (AP1) gene sequence from corn. AP1 is a floral meristem identity product, that promotes conversion of shoot meristem to floral meristem in an angiosperm. Vectors containing the AP1 gene can be used to create transgenic plants. AP1 nucleotide sequences can be used to promote early reproductive development in seed plants can be used to promote early reproductive development in seed plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ92144 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1345 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which is useful for accelerating selective breeding programmes that require several rounds of crossing to produce plants with disease and insect resistance. The nucleotide sequences are particularly useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purified nucleic acids encoding APETALA 1 (AP1) reproductive development in seed plants, useful selective breeding programmes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-181839/16.
P-PSDB; AAY78883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yanofsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6025483-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corn APETALA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoting early reproductive development in long generation seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV
                                                                                                               318
                                                                                                                                                                                                                                                                                                                                                                                                                                                     138
                                                                                                                                                                                                                                                                                                                                                                                             312
378
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                                                                                                                                                                                                                                                                                   372
                                                                                                                                                                                                                                                                                                                                           198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 GAAATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Column 59-62; 50pp; English
                                   AAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGA
                                                                                                                                                                 ACGCCACCGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTG
                                                                                                                                                                                                                            TCCTCTGCGATGCCGAGGTCGCCGTCATCGTCTTCTCCCCCCAAGGGCAAGCTCTACGAGT
                                                                                                                                                                                                                                                         TCCTCTGTGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGT
                                                                                                                                                                                                                                                                                                                                           GGCAGGTGACCTTCTCCAAGCGCCGGAACGGCCTGCTCAAGAAGGCGCACGAGATCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                   GGCAGGTGACCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCAACAAGGCGATGGGGCGCGCCAAGGTACAGCTGAAGCGGATAGAGAACAAGATAAACC
AAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 A; 373 C; 358 G; 265 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.7%;
92.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 300.4; DB 21,
Pred. No. 3.3e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins, promote early for accelerating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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ARAF75
ARF75
ARC AAF75
AC AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kojima
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     TGAAAAGGCTCTTATTTCAGCTGAATCCGAGAGTGAGGGAAATTGGTGCCATGAATACAG
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Query Match
Best Local Similarity
Matches 306; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rice MADS box gene for or agricultural plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice; MADS box;
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a gene which contains the rice MADS box gene. This sequence can be used for regulating plant branching to provide ornamental or agricultural plants. In addition, plants with value-added properties or an increased yield can be produced using the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200114559-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAB73250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-191647/19.
                                                                                                                                                                                                                                                                                                               250 GCGAAATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KUMIAI CHEM KOJIMA M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC
                                                                                                                                                                                                           CAGGCAGGTGACGTTCTCCAAGAGGAGGAATGGATTGCTGAAGAAGGCGCGCACGAGATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 19-20; 43pp; Japanese
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                  TGAAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAG
                                                                                      GTACGCCACCGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCCTACTCTTATGC
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                                                                 GTACGCCACTGACTCCAGGATGGACAAAATCCTTGAACGTTATGAGCGCTATTCATATGC
                                                                                                                                     CGTCCTCTGCGACGCCGAGGTCGCCGCCATCGTCTTCTCCCCCAAGGGCAAGCTCTACGA
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RESULT 12
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Best Local Similarity 91.3%;
Matches 242; Conservative
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16-AUG-1999;
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GGCAGGTGACCTTCTCCAAGCGCCGCAACCGGCTCCTGAAGAAGGCGCACGAGATCTCCG
                          GCAACAAGGCGATGGGGCGCGGCAAGGTACAGCTGAAGCGGATAGAGAACAAGATAAACC
                                       GAAATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGATAGAGAACAAGATAAATC
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RESULT 1
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Query Match
Best Local Similarity
                                                                                                                         cDNA clones SQE1 (AAT34429), SQE2S (AAT34430) and SQE2L (AAT34431) identified by homology to the MADS box of the Arabidopsis apetala 1 (AP1) and Antirrhinum squamosa (SQUA) flower development genes. They were obtd. by PCR amplification of E. globulus DNA using primers based on the MADS box of the Arabidopsis and Antirrhinum genes, followed by screening of a E. globulus young flower bud library. The SQE2S cDNA codes for protein SQE2-S (AAR99635). Antisense or ribozyme constructs of SQE, or of FLE2 and SQE genes (see also AAT34426, AAT34428 and AAT34432), may be used to produce sterile transgenic Eucalyptus trees by minimising inflorescence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eucalyptus; reproductive gene; SQE2S; Arabidopsis; agomous gene; Antirrhinum; plena gene; sterility; fertility; forest tree; transgenic plant; flower development; antisense; ribozyme; ss.
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                                                                             Sequence 1032 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-278411/29
P-PSDB; AAR99635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-1996.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eucalyptus
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dennis ES,
Peacock WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Page 34-35; 60pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; cDNA; 1032
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Southerton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                299 A; 231 C; 263 G; 239 T; 0 other;
  32.9%;
71.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
  Score 195; DB 17; Pred. No. 2.6e-45;
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cDNA clones SQE1 (AAT34429), SQE2S (AAT34430) and SQE2L (AAT34431) identified by homology to the MADS box of the Arabidopsis apetala 1 (AP1) and Antirrhinum squamosa (SQUA) flower development genes.
                                                                                                                     Eucalyptus reproductive Eucalyptus trees useful re-forestation projects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucalyptus; reproductive Antirrhinum; plena gene; transgenic plant; flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT34431 standard; cDNA; 1070
                                                                                    Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-1996
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DB; AAR99636.
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                                                                                                                                                                                                                                                                  k wJ,
                                                                                  Page 36-37; 60pp; English.
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Southerton
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/product= SQE-2L
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184..921
                                                                                                                                          genes - useful for prodn.
for establishing wood lot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; SQE2L; Arabidopsis; agomous gene;
sterility; fertility; forest tree;
development; antisense; ribozyme; ss.
                                                                                                                                                                                                                                                                                     Kyozuka J,
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Best Local Simi
Matches 255;
                25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
23-MAR-1999
25-MAR-1999
01-APR-1999
01-APR-1999
06-APR-1999
16-APR-1999
16-APR-1999
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Antisense or ribozyme constructs of SQE, or of FLEZ and SQE genes (see also AAT34426, AAT34428 and AAT34432), may be used to produce sterile transgenic Eucalyptus trees by minimising inflorescence.
                                                                                                                                                                                                                                                                                                        06-SEP-2000.
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16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;	08-JUL-1999; 09-JUL-1999; 12-JUL-1999; 13-JUL-1999; 14-JUL-1999; 15-JUL-1999; 16-JUL-1999;	1-JUN-19 2-JUN-19 3-JUN-19 3-JUN-19 4-JUN-19 9-JUN-19 0-JUN-19 1-JUL-19 2-JUL-19	18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999;		23 - APR - 1999; 28 - APR - 1999; 28 - APR - 1999; 30 - APR - 1999; 30 - APR - 1999; 05 - MAY - 1999; 06 - MAY - 1999; 07 - MAY - 1999; 11 - MAY - 1999; 12 - MAY - 1999; 13 - MAY - 1999; 14 - MAY - 1999; 17 - MAY - 1999; 18 - MAY - 1999; 19 - MAY - 1999; 21 - MAY - 1999;
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Matches 244; Conservative
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                                                        499 TCTTATTTCAGCTGAAACTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAA 558
                                                                                                                                            379 TGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCAC
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Search completed: June 29, 2003, 07:29:46 Job time : 162 secs THIS PAGE BLANK (USPTO)

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Result
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Sequence 11, Appl	e 11,		Sequence 11, Appl	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	1,	16	14	54		-	Sequence 9, Appli	Sequence 9, Appli	е 9,	•	Sequence 5, Appli

ALIGNMENTS

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COMPUTER: INM PC-POS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 336
ATTORNEY/AGENT INFORMATION:
ARBITISTRATION UNMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION UMBER: 9-UD 1927
TELECOMMUNICATION UMBER: 35-9001
TELEFHONE: (619) 535-9001
TELEFHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 base pairs
TYPE: mucleic acid
CTMPANTENNESS: Anible
                                                              US-08-592-214A-7
Query Match
Best Local Similarity
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                                                                          FEATURE: misc_feature
NAME/KEY: misc_feature
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LOCATION:
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell and Flores
4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States
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                                                                                                                                                        CDS
149..968
                                                                                                                                                                                                                    cDNA
                                                                                                                                                                                                                                                      double
    50.7%;
92.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cauliflower Floral
    Score 300.4; DB 1;
Pred. No. 1.3e-74;
                                                                              Zea mays AP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suite
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                      Length 1345;
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US-08-659-188-7
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                                                                                                                                                                                              TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                 EATURE:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 05-JUN CLASSIFICATION: 800
                                                                 LOCATION:
                                                                                NAME/KEY:
                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 92122
                  NAME/KEY:
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 OTHER INFORMATION:
                                                                                                                                 TOPOLOGY:
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California
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4370 La Jolla Village
                                                                                                                                                                             1345 base pairs
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               misc_feature
1..1345
                                                                149..968
                                                                                CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
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/note= "product =
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US-08-655-227-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                               TELEFAX: (619) 535-89
(NFORMATION FOR SEQ ID NO:
                                                                                                                                                                            NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                FEATURE:
                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         STRANDEDNESS:
                                                                                              LENGTH: 1345 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 05-JU
                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
               NAME/KEY:
LOCATION:
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California
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                                                                linear
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                                               CDNA
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                                                                              double
                                                                                                                                                               535-8949
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suite 700
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NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 896
; TYPE: DNA
ORGANISM: Arabidopsis sp.
; FEATURE:
; PATURE: (7): (753)
; COCATION: (7): (753)
OTHER INFORMATION: AGAMOUS-LIKE 1 (AGL1)
US-09-978-729A-3
Search completed: June 29, 2003, 07:52:55 Job time: 111 secs
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US-09-978-729A-3
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Best Local Similarity 61.3%;
Matches 165; Conservative
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CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yanofsky, Martin F. APPLICANT: Liljegren, Sarah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Liljegren, Sarah
PPLICANT: The Regents of the University of California
ITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
ITLE OF INVENTION: Plants
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ent No. US20020178465A1
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                                                                                   CTCCTTCCGTCACCGAAGCTAATACTCAG 315
                                                                                                                           CTCTTATTTCAGCTGAATCTGAAAGTGAG 526
                                                                                                                                                                   ACAACAGTGTGAGGGGTACAATTGAAAGGTACAAGAAAGCTTGTTCCGATGCCGTCAACC 286
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Pred. No. 1.5e-22;
0; Mismatches 104;
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Sequence 13, Application US/09853450 Publication No. US20020194645A1

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; Sequence 27, Application US/09853450; Publication No. US20020194645A1; GENERAL INFORMATION:
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                  SOFTWARE: PATE SEQ ID NO 27 LENGTH: 747 TYPE: DNA
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 756
TYPE: DNA
ORGANISM: Brassica oleracea var. botrytis
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Matches
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APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
                                                                           TITLE OF INVENTION: Combinations of Genes
TITLE OF INVENTION: Exhibiting Mcdulated
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver: 2.1
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NAME/KEY: CDS
LOCATION: (1)..(453)
OTHER INFORMATION: CAULIFLOWER
ORGANISM: Arabidopsis thaliana
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208; Conserv
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Ditta, Gary
The Regents of the University of California
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Pred. No. 8e-3:
0; Mismatches
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8e-32;
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, LUCATION: (1)..(747)
; OTHER INFORMATION: SEPALLATA1 (SEP1)
US-09-853-450-27
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                                                                                                                                                                                                                                                                                                                         SEQ ID NO 29
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Best Local
                                                                                                                          Matches 188;
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yanofsky, Martin F. APPLICANT: Pelaz, Soraya
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                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 61
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: (1)..(753)
OTHER INFORMATION: S
                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                      LENGTH: 753
                                                                                                                                           Local Similarity
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Similarity 60.1%;
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                              TTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGAC
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Ditta, Gary
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                                                                                                                            Conservative
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                                                                                                                                                                                                           SEPALLATA2 (SEP2)
                                                                                                                                          18.5%;
                                                                                                                         Score 110; DB 9; L
Pred. No. 5.7e-25;
0; Mismatches 130;
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Pred. No. 1.7e-26;
0; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                    of California
for Producing Seed Plants
Reproductive Development
                                                                                                                                                          Length 753;
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Sequence 9, Application US/09853450
; Publication No. US20020194645A1
; GENERAL INFORMATION:
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                                                                                                                                                                                      Query Match
Best Local S
Matches 226
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SEQ ID NO 9
LENCTH: 779
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: The Regents of the University of California TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants TITLE OF INVENTION: Exhibiting Modulated Reproductive Development FILE REFERENCE: 19452A-002400US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yanofsky, Martin F. APPLICANT: Pelaz, Soraya
                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: (10)..(777)
LOCATION: CAULIFLOWER (CAL)
OTHER INFORMATION: CAULIFLOWER (CAL)
NAME/KEY: modified base
LOCATION: (778)..(779)
OCHER INFORMATION: n = 9, a, c or t
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                      Local Similarity
nes 226; Conserv
380
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                                                                                                                                   260 GATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTG
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GACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCACC
                                                                      ACCITCICCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGT 379
                                                                                                           GAAATGGGAAGGGGTAGGGTTGAATTGAAGAGATAGAGAACAAGATCAATAGACAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGAAGTTGCGCTTGTTGTCTCCCCATAAGGGGAAACTCTTTGAATACCCCACTGAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCACCGAC 442
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Ditta, Gary
                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                        24.5%; Score 145.2; DB 9; 66.5%; Pred. No. 3.1e-36;
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67.1%;
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Pred. No. 6.8e-40;
                                                                                                                                                                                        Mismatches
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US-09-853-450-11
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Best Local S
Matches 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (1).
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APPLICANT: Pelaz, Soraya
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TYPE: DNA
ORGANISM: Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION:
 301
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 AAGGCTAAGATTGAGCTTTTGGAGAGAAACCAAAGGC
                                AAGGCGAAGATTGAGACCATACAAAATGTCACAAGC
                                                                  AAAGTTCCAGACTCTCACGTCAATGCACAAACGAACTGGTCAGTGGAATATAGCAGGCTT
                                                                                                  ATTTCAGCTGAATCTGAAAGTGAGGGA-----AATTGGTGCCACGAATACAGGAAACTT
                                                                                                                                      TCTTGCATGGAGAAGGTACTAGAACACTACGAGAGGTACTCTTACGCCGAGAAACAGCTA
                                                                                                                                                                      TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT
                                                                                                                                                                                                          GCTGAGGTTTCCCTTATTGTCTTCTCCCATAAGGGGAAACTGTTCGAGTACTCGTCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAAGGCT 499
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0; Mismatches 114;
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337
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RESULT 12 US-09-853-450-13

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; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-740A-1
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                                                            Sequence 1, Application US/09978730
Patent No. US20020129403A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Maxtin F.
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LENGTH: 1062
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 19452A-000960US
CURRENT APPLICATION NUMBER: US/09/978,740A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
APPLICANT: Liljegren, Sarah
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Liljegren, Sarah
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynt
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yanofsky, Martin F. APPLICANT: Liljegren, Sarah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                           GCGAAGATTGAG 571
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Pred. No. 2.1e-40;
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, NAME/KEY: CDS
; LOCATION: (101)...(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-730-1
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US-09-853-450-5
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                                                                                                                                                                                                                                                     APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of Producing Seed Plants

---- On INVENTION: Combinations of Genes for Producing Seed Plants

---- Marting Modulated Reproductive Development
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Best Local (
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                                                                                                                                                       SEQ ID NO 5
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FILE REFERENCE: 19452A-000920US
CURRENT APPLICATION NUMBER: US/09/978,730
CURRENT FILING DATE: 2001-10-15
- PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR APPLICATION NUMBER: US 09/339,998
                                                                                                                                                                     TITLE OF INVENTION: Combinations of Genes
TITLE OF INVENTION: Exhibiting Modulated
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.1
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NUMBER OF SEQ ID NOS: 25
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NAME/KEY: CDS
LOCATION: (1)..(768)
OTHER INFORMATION: APETALA1 (AP1)
                                                                TYPE: DNA ORGANISM: Brassica oleracea var. botrytis FEATURE:
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al Similarity 69.2%;
216; Conservative
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Pred. No. 2.1e-40;
0; Mismatches 96;
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APPLICANT: Farrandiz, Cristina
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
APPLICATION: Selective Control of Lignin Biosynthesis in
TITLE OF INVENTION: Plants
FILE REFERENCE: 19452A-000940US
CURRENT APPLICATION NUMBER: US/09/981,087A
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
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; NAME/KEY: CDS
; LOCATION: (101)..(829)
; OTHER INFORMATION: AGAMOUS-LIKE 8
US-09-978-729A-1
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US-09-981-087A-1
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                                                                   Matches
                                                                                   Query Match
Best Local (
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Best Local
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                                                                                                                                                    FEATURE: FEATURE: LOCATION: (101)...(829)
OTHER INFORMATION: AGAMOUS-LIKE 8
                                                                                                                                                                                                                    ORGANISM: Arabidopsis
                                                                                                                                                                                                                                           LENGTH: 1062
TYPE: DNA
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                        GATATGGGTCGCGGCAAGGTGCAGGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTG 319
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GATATGGGAAGAGGTAGGGTTCAGCTGAAGAGGATAGAGAACAAGATCAATAGGCAAGTT
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Farrandiz, Cristina
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                                                                Score 158.4; DB 9
Pred. No. 2.1e-40;
0; Mismatches 96
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Pred. No. 2.1e-40;
0; Mismatches 96
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157
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FEATURE:
NAME/KEY: CDS
LOCATION: (101)...(829)
COTHER INFORMATION: AGAMOUS-LIKE 8 (AGL8)
US-09-978-382A-1
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Best Local S
Matches 216
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APPLICANT: Liljegren, Sarah
APPLICANT: Liljegren, Sarah
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
TITLE OF INVENTION: Plants
CURRENT FOR NUMBER: US/09/978,382A
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1998-06-25
PRIOR PILING DATE: 1999-06-25
PRIOR PILING DATE: 1999-06-25
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ORGANISM: Arabidopsis
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 CTTGTTGGCCGAGACGTTTCACAAAGTGAAAATTGGGTTCTAGAACATGCTAAGCTCAAG
                              CTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAG
                                                                     GACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAAGGCT
                                                                                                                                            GATGCTGAGGTTGCTCTCATCGTCTTCTCTTCCAAAGGCAAACTCTTCGAATATTCCACC
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Pred. No. 2.1e-40;
0; Mismatches 96
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US-09-853-450-1
                                                    RESULT 3
US-09-853-450-3
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Sequence 3, Application US/09853450 Publication No. US20020194645A1 GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 1
LENGTH: 1057
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APPLICANT:
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ~ID NOS: 61
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TITLE OF INVENTION: Exhibiting Modulated
FILE REFERENCE: 19452A-002400US
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ORGANISM: Arabidopsis thaliana
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LOCATION: (124)..(894)
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Ditta, Gary
The Regents of the University of California
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Pred. No. 5.3e-42;
0; Mismatches 106
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; LOCATION: (36)..(79
; OTHER INFORMATION:
US-09-853-450-3
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                                                       NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. :
SEQ ID NO 1
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APPLICANT: Yanofsky, Martin F.
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09978729A Patent No. US20020178465A1
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                                                                                                                                                                                  APPLICANT: Liljegren, Sarah
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
TITLE OF INVENTION: Plants
FILE REFERENCE: 19452A-000950US
CURRENT EPPLICATION NUMBER: US/09/978,729A
CURRENT FILING DATE: 2002-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
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                                                                                                         PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
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APPLICANT: Pelaz, Soraya
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TYPE: DNA ORGANISM: Arabidopsis sp.
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Ditta, Gary
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15,	67,		Sequence 160, App	Sequence 9, Appli	Sequence 19, Appl	Sequence 44, Appl	13	15	Sequence 42, Appl	Sequence 43, Appl	Sequence 9686, Ap	Sequence 718, App	Sequence 31, Appl	Sequence 1, Appli	Sequence 3783, Ap	Sequence 14, Appl	æ	Sequence 542, App	Sequence 848, App	4	ნ	ე	<u>ა</u>	ູຫ	Sequence 5, Appli

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APPLICANT: Yanofsky, Martin F.
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Best Local Similarity
Matches 316; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 7
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University
TITLE OF INVENTION: Combinations of Genes
TITLE OF INVENTION: Exhibiting Modulated
FILE REFERENCE: 19452A-002400US
                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: CDS
LOCATION: (149).. (970)
OTHER INFORMATION: APETALA1 (AP1)
                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1345
                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                               198
                                                                                                312
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258
                               372
                                                                                                                                                                   252 GAAATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATC
                                                                                    GGCAGGTGACCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCCG
 TCCTCTGCGATGCCGAGGTCGCCGTCATCGTCTTCTCCCCCAAGGGCAAGCTCTACGAGT
                   TCCTCTGTGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGT
                                                                GGCAGGTGACCTTCTCCAAGCGCCGGAACGGCCTGCTCAAGAAGGCCGCACGAGATCTCCG
                                                                                                                                 GCAACAAGGCGATGGGGCGCGGCAAGGTACAGCTGAAGCGGATAGAGAACAAGATAAACC
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                  50.7%;
                                                                                                                                                                                                    0;
                                                                                                                                                                                                                  Score 300.4;
Pred. No. 7.6
                                                                                                                                                                                                      Mismatches
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for Producing Seed Plants
Reproductive Development
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                                                                                                                                                                                                                                    Length 1345;
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317
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Sequence Sequence

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                                                      Query Match
Best Local Sim:
Matches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 794 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application Patent No. 6002069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -08-659-188-3
                                                                                                                                                                                                                                                                                                                                                                                               RAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-UUN-1996
CLASSIFICATION: 800
                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                        MOLECULE TYPE: cDNA .
                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                     NAME/KEY: misc feature LOCATION: 1.794
OTHER INFORMATION: /not OTHER INFORMATION: AP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
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261 ATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGA 320
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T: 4370 La Jolla Village Drive, Suite 700
San Diego
California
                                                    Similarity 67.3
24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTC 500
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36..794
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                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                       double
                                                                     26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Martin F.
Seed Plants Exhibiting Inducible Early
Reproductive Development and Methods of Making Same
                                                                                                                                      /note= "product = Brassica oleracea
AP1."
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                                                                    Pred. No. 4e-35;
                                                    Mismatches 109;
                                                    Indels
                                                                                   Length
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                                                                                                              501
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334 CTAAGATTGAGCTTTTGGAGAGAAACCAGAGGC 366
                                    561 CGAAGATTGAGACCATACAAAAATGTCACAAGC
                                                                                                                                                                                    441 ACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTC
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                                                                                                            TTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGG 560
                                                                                                                                                 ATTCTTGTATGGAGAAGATACTTGAACGCTATGAGAGATACTCTTACGCCGAGAGACAGC
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Search completed: June 29, 2003, 07:26:47 Job time : 36 secs

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US-09-149-976-1
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                                                                                                                                                                                                  Matches 227;
                                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                 LOCATION: 1..1215
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/00 FILING DATE: 09-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
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No. 6127123
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259
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                                                                                  CCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTG 380
                                                                                                                               AAATGGGAAGGGGTAGGGTTCAATTGAAGAGATAGAGAACAAGATCAATAGACAAGTGA
                                                                                                                                                             АТАТGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGA 320
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                             ACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCACCG 440
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1215 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           United States
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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68.2%;
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thaliana AP1"
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                                                                                                                                                                                                              Score 163.4; DB 3; Pred. No. 2.2e-36;
                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                              106;
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RESULT 14
US-08-592-214A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Yanofs
                                                                                                                                                     Query Match
                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (619) 535-89.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 794 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619)
                                                                                                                                                                                                   LOCATION: 1..794
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: 1..794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Campbell, Cath
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 26-JAN CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: San Diego
STATE: California
                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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                                                                                        261 ATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGA
94
                                                           34 AAATGGGAAGGGGTAGGGTTCAGTTGAAGAGGATAGAAAACAAGATCAATAGACAAGTGA
                                                                                                                                     h 26.7%;
Similarity 67.3%;
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                       CCTTCTCCAAGCGCCCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCCGTCCTCTGTG
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CATTCTCGAAAAGAAGAGCTGGTCTTATGAAGAAAGCTCATGAGATCTCTGTTCTGTGTG
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36..794
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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AP1"
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                                                                                                                       Score 158.6; DE
Pred. No. 4e-35;
0; Mismatches 1
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                                                                                                                                                       DB 1;
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NAME/KEY: misc feature

LOCATION: 1..1057

OTHER INFORMATION: /note

OTHER INFORMATION: thali
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APPLICATION NUMBER: US 0:
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 3739
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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             CTAAGATTGAGCTTTTGGAGAGAAACCAGAGGC
                                    CGAAGATTGAGACCATACAAAAATGTCACAAGC 593
                                                                      TTATTGCACCTGAGTCCGACGTCAATACAAACTGGTCGATGGAGTATAACAGGCTTAAGG
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                                                                                                 TTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGG
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thaliana AP1."
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la Village Drive
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Pred. No. 2e-
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Best Local S
Matches 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1215 base pair
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CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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LOCATION:
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TTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGG
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                                                                       ACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTC
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4370 La Jolla Village
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SYSTEM: PC-DOS/MS-DOS
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thaliana AP1"
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Pred. No. 2.2e-36;
0; Mismatches. 106;
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READABLE FORM:

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Patent No. 6025543
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                                                                                                                  GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
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CURRENT APPLICATION DATA:
                                                                                 APPLICANT:
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                                                TITLE OF INVENTION:
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                 NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
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OPERATING SYSTEM: PC-DOS/MS-DOS
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LOCATION: 1..1057
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CLASSIFICATION:
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STRANDEDNESS: double
 ADDRESSEE:
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                                                                                               Yanofsky, Martin F.
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Campbell and Flores
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                                                Seed Plants Exhibiting Early Reproductive Development and Methods of Making Same
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thaliana AP1."
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RESULT 11
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Matches 2
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SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,015
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
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MEDIUM TYPE: Floppy disk
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LOCATION: 1..1057
OTHER INFORMATION: /note= "product = OTHER INFORMATION: thaliana AP1."
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CLASSIFICATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                               CTAAGATTGAGCTTTTGGAGAGAAACCAGAGGC
                                                                                             CGAAGATTGAGACCATACAAAAATGTCACAAGC
                                                                                                                            TTATTGCACCTGAGTCCGACGTCAATACAAACTGGTCGATGGAGTATAACAGGCTTAAGG
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N: CLASS 800
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Pred. No. 2e-36;
0; Mismatches 106;
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Sequence 1, Application US/09398326
Patent No. 6355863
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants

Exhibiting Inducible Early

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Best Local Similarity
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TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US, FILING DATE: 12-21-95 CLASSIFICATION: 800 PRIOR APPLICATION NUMBER: 08, FILING DATE: 12-21-94
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                             APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07
                                                                                                                                              STREET:
   OPERATING SYSTEM:
                                                                                        COUNTRY:
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                                                                                                           San Diego
California
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                                                                                                                                              E: Campbell and Flores
4370 La Jolla Village
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68.2%;
compatible
PC-DOS/MS-DOS
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                                                                                                                                          Village Drive,
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                                                                                                                         Sequence 1, Application U$/08655227
Patent No. 6025483
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Maize and Cc
TITLE OF INVENTION: Products and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                           CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,188
                                                                                                            NUMBER OF SEQUENCES:
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LOCATION:
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OTHER INFORMATION: /noi
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                                                               STREET:
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              COUNTRY:
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                             San Diego
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                                                           4370 La Jolla Village Drive, Suite 700
                USA
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                                                                            Campbell and Flores
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Maize and Cauliflower APETALA1 Gene
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Pred. No. 2e-3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                   equence 7, Application US/09398326 etent No. 6355863
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                          APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting Inducible Early
TITLE OF INVENTION: Reproductive Development and Methods of Making Same
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OTHER INFORMATION: /no
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STRANDEDNESS: double
                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
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                                                   APPLICATION NUMBER:
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APPLICATION DATA:
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Pred. No. 1.3e-74;
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                                                                                     Version #1.
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                                                                                                                                                                                                                                             Sequence 1,
Patent No. 5
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Best Local
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INFORMATION FOR SEQ ID NO:
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NAME/KEY:
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LENGTH: 1345 base pairs
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               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                            APPLICANT: Weigel, Detlef TITLE OF INVENTION: Genet TITLE OF INVENTION: Flowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                NUMBER OF SEQUENCES:
                                              STATE: CA
COUNTRY: US
ZIP: 92037
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OTHER INFORMATION:
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STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                              CITY: La Jolla
COMPUTER:
                                                                                                ADDRESSEE: Fish & RICHARDSUM .... STREET: 4225 Executive Square, Suite 1400
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                                                                                                                                                                                                                                                 , Application US/08576156 5844119
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US
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IBM Compatible
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31,815
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Pred. No. 1.3e-74;
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US-08-655-241-7
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APPLICANT: Yanofsky, Mar
APPLICANT: Weigel, Detle
TITLE OF INVENTION: Seed
TITLE OF INVENTION: Deve
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08655241 Patent No. 6025543
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Best Local Similarity
Matches 316; Conserv
                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                             APPLICATION NUMBER: US/08/
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
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LOCATION: 1.1345
OTHER INFORMATION: /note= "product = Zea mays AP1."
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                LENGTH:
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: California
: 1345 base pairs nucleic acid
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Weigel, Detlef
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Pred. No. 1.3
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RESULT 5
US-09-149-976-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/09149976 Patent No. 6127123
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Best Local Similarity
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APPLICANT: Yanofsky
TITLE OF INVENTION:
TITLE OF INVENTION:
                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMER: US 08/5:
FILING DATE: 26-JAN-1996
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNMER: 31,815
REFERENCE/DOCKET NUMBER: P-1
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/149,976

FILING DATE: 09-SEP-1998

CLASCIPTATION OF THE OPERATION OF T
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TELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ALIGNMENTS

	source 1	FEATURES L	Email: tsh	Fax: 81-559-81-6855	Tel: 81-55	1111 Yata,	National I	Center For	COMMENT Contact: T	JOURNAL Unpublishe	TITLE Expressed	AUTHORS Ogihara, Y.	REFERENCE 1 (bases	; Triticea	Spermatoph	Eukaryota;	ORGANISM Triticum aestivum	SOURCE bread wheat.	KEYWORDS EST.	VERSION BJ208073.1	ACCESSION BJ208073	cDNA clone	DEFINITION BJ208073 Y	LOCUS BJ208073	ВJ208073	
<pre>'Organism="Triticum aestivum" 'Cultivar="Chinese Spring" 'db_xref="taxon:4565"</pre>	633	Location/Qualifiers	Email: tshini@genes.nig.ac.jp.	9-81-6855	81-559-81-6856	1111 Yata, Mishima, Shizuoka 411-8540, Japan	National Institute of Genetics	Center For Genetic Resource Information	Contact: Tadasu Shin-i	Unpublished (2002)	genes in Triticum aestivum	Ogihara,Y. and Murai,K.	(bases 1 to 633)	le; Triticum.	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	lestivum	ī r .		BJ208073.1 GI:19946124		cDNA clone wh6110 5', mRNA sequence.	library, Wh Tri	633 bp mRNA linear EST 04-APR-2002		

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Query Match
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
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tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Xianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
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/tissue_type="spike at meiosis"
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Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540,
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Contact: Tadasu Shin-i
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Ogihara, Y. and Murai, K.
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TGCGCGCCATAGACACAAGAGCCGACAGCTAGATCGCGAAATCAGGATATGGGTCGCGGC
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81-559-81-6855
                                                                                                                                                                                                                                                                                              /clone="wh5m21"
/clone lib="Y. Ogihara unpublished cDNA library, Wh"
/tissue_type="spike at meiosis"
/dev stage="Feekes' scale 9"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
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samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                           Conservative
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Location/Qualifiers
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/db_xref="taxon:4565"
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
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Ogihara, Y. and Murai, K.
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                                         CATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCACCGACTCCAGCATGGACAA 456
                                                                                                                                                                                    CAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGACGCGGAGGTCGCCGT 396
                                                                                                                                                                                                                                                                                                                               GGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACCTTCTCCAAGCGCCG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                 CGCGCCATAGACACAAGAGCCGACAGCTAGATCGCGAAATCAGG--ATGGGTCGCGGCAA 137
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/note="vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
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tissue, equal quantities of RNA were pooled from the two
samples, polya was purified from the pooled RNA, a cDNA
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excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
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Location/Qualifiers
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Plasmid DNA preparations and DNA
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/tissue_type="spikelet at late flowering"
/dev_stage="Feekes' scale 6"
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db_xref="taxon:4565"
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99.3%;
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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fo., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Seaton,C.L. and Tong,J.C:
The structure and function of the expressed portion of the expressed portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE500707 492 bp mRNA linear EST 04-AUG-2000 WHE0991-0994 I21 I21ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE0991-0994 I21 I21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta;
; Triticeae; Triticum.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACAAAAATGTCACAAGC
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                                                                                                   poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                         /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EccRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white,
and yellow anther were collected and total RNA, and
                                                                                                                                                                                                                                                                                                                                             /clone="WHE0991-0994_I21_I21"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli_SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cultivar="Chinese Spring"
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                  67.8%;
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Score 402; DB 10;
Pred. No. 1.5e-93;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                Contact: Olin Anderson
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                      quality sequence with phred score
Seq primer: Stratagene SK primer.
Location/Qualifiers
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Anderson,O.D., Choo,S., Choi,D.W., Close,T.J., Fe,P.S., Hsia.C.C., Kang,Y., Lazo,G.R., Miller,R., Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portigenomes - Pre-anthesis spike cDNA library Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aestivum cDNA
BG605208
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                                                                                                                                                                                                                                                                                                                                                           800 Buchanan Street, Tel: 5105595773
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                                                                                                                                                                                                                                                                                                        Sequence have been trimmed to
                                                                                                                                                                                                                                                                                                                          Email: oandersn@pw.usda.gov
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/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript
                                                                                                    /clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli_SOLR"
                                                                                                                                                                          /db_xref="Chinese Spring"
/db_xref="taxon:4565"
/clone="www.accorder.com"
                                                                                                                                                                                                       organism="Triticum aestivum"
|cultivar="Chinese Spring"
                                                                                                                                                                        clone="WHE2330 A04 A08"
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180 CAGCGACGTCTCGCCTCCCCACCCCGGCCGCCGTGCGCGCCATAGACACAAGAGCCGA
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                                                                                                                                                                                                                                      BJ316394 Y. Ogihara aestivum cDNA clone
                                                   1 (bases 1 to 691)
Ogihara, Y. and Murai, K.
                                                                                        Spermatophyta; Magnoliophyta; ; Triticeae; Triticum.
                                                                                                                                             Triticum aestivum
Contact: Tadasu Shin-i
             Expressed genes in Triticum Unpublished (2002)
                                                                                                                            Eukaryota; Viridiplantae;
                                                                                                                                                                 bread wheat.
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98.8%;
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a unpublished cD
whyf22009 5', '
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Pred. No. 8.8e-92;
0; Mismatches 3
                                                                                                           Streptophyta; En
/ta; Liliopsida;
                                    aestivum
                                                                                                                                                                                                                          mkNA linear EST 09-APR-2002 CDNA library, Wh_yf Triticum', mRNA sequence.
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Riverside. Plasmid Di
g were performed in t
                                                                                                           Embryophyta; Tracheophyta;
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
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                                                                                                                                                                                                                                                                 81-559-81-6855
                                                                                                                                                                                                          tshini@genes.nig.ac.j
Location/Qualifiers
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whyf22009"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh_yf"
/tissue_type="spikelet at early flowering"
/dev_stage="Feekes' scale 6"
                                                                                                                                                           organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                   Japan
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REFERENCE
AUTHORS
TITLE
                                                                                                                                JOURNAL COMMENT
                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
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ORIGIN
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8J212134
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                                       Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6856
                                                                                                                         1 (bases 1 to 694)
Ogihara,Y. and Murai,K.
Expressed genes in Triticum
Unpublished (2002)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                  cDNA clone wh34p04 5',
BJ212134
                                                                                                                                                                                                                                                                                                                                                                                                                            BJ212134
BJ212134 Y.
                                                                                                                                                                                                                                                                                                 Triticum aestivum
                                                                                                                                                                                                                                                                                                                         bread wheat.
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                        81-559-81-6855
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tshini@genes.nig.ac.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown unde
hydroponic conditions at UC Davis, salt stressed f
                                                                                                                                                                                                                                                                                                                                                                                                    694 bp mRNA lir
Ogihara unpublished cDNA library,
wh34p04 5', mRNA sequence.
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Pred. No. 1.2e-91;
0; Mismatches 2;
                                                                                                                                                                       aestivum
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a; Poales; Poaceae; Pooideae
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SOURCE

Kleinhofs, A., Wise, R.,

Chin, A.,

FOCUS

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REFERENCE
AUTHORS
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HVSWERD0001F21f Hordeum vulgare r.
(normal) Hordeum vulgare cDNA cli
B1956235
B1956235.1 GI:16306797
Hordeum vulgare Eukaryota; Viridiplantae; Streptophyta; En Spermatophyta; Magnoliophyta; Liliopsida; Triticeae; Hordeum.

1 (bases 1 to 1196)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R.
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                                                                                                                        Hordeum vulgare.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="spike at meiosis"
//dev_stage="Feekee' scale 9"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EccRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples; polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
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/clone_lib="Y. O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:4565"
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99.0%;
                                                                                                                                                                                                vulgare cDNA clone HVSMEn0001F21f,
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Pred. No. 1.2
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rachis EST library HVcDNA0015
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                                                                Embryophyta; Trach
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                                                                                                                                                                                                    mRNA sequence
                                                                                Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 410;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for barley genomics: Morex rachis Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmo,J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total hg bases = 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
  CGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCACCGACTCCAGCATGGACAAAAT 459
                                                                                 CGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGACGCGGAGGTCGCCGTCAT 399
                                                                                                                                                                                    GCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACCTTCTCCAAGCGCCCCAA 339
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                                                                                                                                                                                                                                                                                                                                                                                        GCANCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACCTTCTCCAAGCGCCGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pullman, WA in a greenhouse, the rachises were excised and frozen in liquid nitrogen (Kleinhofs lab). In the TJ Close lab at the University of California, Riverside total RNA was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and I million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rwing@clemson.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html) "
a 439 c 270 g 172 t 37 others
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XhoI; Plants were grown at Washington State University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_lib="Hordeum vulgare rachis EST library HVcDNA0015"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="taxon:4513"
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94.5%;
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Pred. No. 2.7e-89;
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Best Local (
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                                                                                       409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               658 bp mRNA linear EST 04-APR-200;
BJ213269 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
cDNA clone wh21]22 5', mRNA sequence.
BJ213269
a
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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Triticem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expressed genes in Triticum Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogihara, Y. and Murai, K.
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                                       GCGACGTCTCGCCTCCCCACCCCGGCCGCCGTGCGCGCCATAG-ACACAGAGCCGAC
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81-559-81-6855
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/clone lib="". Ogihara unpublished cDNA library, Wh"
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kiannian, Otto, Simons, Zhang).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."
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                                                                                       Conservative
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Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
West Area, Western Albany, CA 94710, USA
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The structure and function of the expressed portigenomes - Pre-anthesis spike cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oandersn@pw.usda.gov
                     inote="vector: Lambda Uni-ZAP XR, excised phagemid; site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pbluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at
                                                                                                                                                                                                                        /clone_lib="Wheat pre-anthesis spike cDNA library"
/clssue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E_coli_SOLR"
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                                                                                                                                                                                                                                                                                          Development of a genetically and physically anchored EST for barley genomics: Morex rachis cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
; Triticeae; Hordeum.
                                                                                                                                  Email: rwing@clemson.edu
Total hq bases = 419
                                                                                                                                                                        100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                      Wing,R., Close,T.J., Kleinhofs,A., Wise, Frisch,D., Atkins,M., Yu,Y., Henry,D., F
                                                                                                                                                                                                                                                                            Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hordeum vulgare.
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lemson University
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Location/Qualifiers
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Anderson lab (all other authors)."
1 141.c 143 g 105 t
                  organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
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clone HVSMEn0010B09f, mRNA sequence.
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                                                                     BJ211202 623 bp mRNA lir
BJ211202 Y. Ogihara unpublished cDNA library,
cDNA clone wh38g11 5', mRNA sequence.
BJ211202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was prepared, poly(A) was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pbluescript SK(-) cDNA phagemids (Chin). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or book for the sequence and contains a minimum of 100 bases of phred value 20 or book for the sequence and contains a minimum of 100 bases of phred value 20 or book for the sequence and contains a minimum of 100 bases of phred value 20 or book for the sequence and the sequence 
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http://www.genome.clemson.edu/projects/barley.
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/lab_host="TJC121"
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SOURCE

DEFINITION

BQ778659 572 bp mRNA linear EST 26-JU 946113A11.yl 946 - tassel primordium prepared by Schmidt lab

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expressed genes in Triticum Unpublished (2002)
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Ogihara, Y. and Murai, K.
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                                                                                                                         TTGAGACCATACAAAAATGTCACAAGC 593
                                                                                                                                                                               CAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCGAAGA
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                                                                                                                                                                                                                                                                                                                                            AGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCACCCGACTCCA
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Site 1: BCORI; Site 2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the TJ Close lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang)
. Choi, Close, Fenton, Kianian, Otto, Simons, Zhang)
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson lab (all other authors)."

95 a 158 c 165 g 102 t 3 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="wh38g11"
/clone_lib="Y. Ogihara unpublished cDNA library,
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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Pred. No. 1.4e
0; Mismatches
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a: Poales; Poaceae; Pooideae
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BQ778659
BQ778659.1
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Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 227
Fax: 650 725 8221
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1 (bases 1 to 572)
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Location/Qualifiers
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               TCTTATGCTGAAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCAC
                                                               CTCTATGAGTACGCCACCGACTCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTAC
                                                                                              GAGATETECETETECGAEGECEGAEGTEGECETEATEGTETETECECECAAGGGCAAG
                                                                                                                    GAGATCTCCGTCCTCTGTGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAG
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                                                                                                                                                                                                                                             CCTCCCCTGATCCCCTCTTCACATCCTACCACCTCTTTAAAGCTACCCAGCTACCTGCCT 109
                                                                                                                                                                     AAGATAAATCGGCAGGTGACCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Zea mays"
/cultivar="OH43"
/db_xref="taxon:4577"
/clone_lib="946 - tasse
                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the clibrary in HybriZAP. Sample insert size range was 35 to 3 Kb with a 1 Kb average."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="just after the transition
inflorescence development"
/lab_host="XLOLR"
                                                                                                                                                                                              -GAGGCAGGCGAAGATGGGGCGCGCCAAGGTGCAGCTGAAGCGGATAGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissue_type="tassels"
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Pred. No. 3.6e-68;
0; Mismatches 95;
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AACTGAAGGCCAAAATTGAGACCATACNNNNNTGCCACAAGC
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Best Local Similarity
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
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                                                                                                                                                                                                                                           TCCTCTGTGACGCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGT
                                                                                                                                                                                                                                                                                                                              GGCAGGTGACCTTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCCG
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AACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAGC
                                                                     AAAAGGCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGA
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Mapping Project 292 g 238 t 385 others
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/db_xref="MaizeDB:630908"
/db_xref="taxon:4577"
/clone="CL2300_1"
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89.5%;
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Pred. No. 1.6e-64;
0; Mismatches 36
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JOURNAL
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Best Local Similarity
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Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             An EST database from Sorghum: ovaries of varying immature stages Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: JEN REV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sorghum bicolor
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                                                                                                                     GGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGACGCGGAGGTCGCCGTCATCG 401
                                                                                                                                                                                                                                           CTAGCGCAGCAAGCGCCCATCAGCAAGCAGATCGGAGCAAGATGGGGCGCGCCAAGGTGC
                                                                                                                                                                                                                                                                                   AGCCGACAGCTAGATCGCGAAATCAGG-----ATATGGGTCGCGGCAAGGTGC 281
                                                                                                                                                               AGCTCAAGCGGATAGAGAACAAGATAAACCGGCAGGTGACCTTCTCCAAGCGCCGCAACG
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/note="Organ: Mix of ovaries of varying immature stages from 8 week-old plants; Vector: pBluescript II from Lambda Zap II, Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.

Clones to be sequenced were prepared by mass excision."

155 c 121 g 83 t
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/db_xref="taxon:4558"
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Pred. No. 5.5e-62;
0; Mismatches 95;
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Search completed: June 29,
                                                                        522 GTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCGAAGAT 567
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                                                     GTGAGGGAAACTGGTGCCACGAATACAGGAAACTGAAGGCCAAAAT
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Percent Similarity:
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                                                             RESULT 15
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Pfam; PF001486; SF-TF; 1.
Pfam; PF00319; SFF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS BOX 1; 1
PROSITE; PS50066; MADS BOX 2; 1
PROSITE; PS50066; MADS BOX 2; 1
DNA-binding; Nuclear protein; T
SEQUENCE 244 AA; 28093 MW;
 Q39399;
Q39399;
01-NOV-1996
01-NOV-1996
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-!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS
EMBL; AJ249144; CAB97352.1; -.
HSSP: D11746. 12074
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Triticeae; Hordeum.
TRII_TaxID=4513;
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MEDLINE=20346590; PubMed=10890536;
Schmitz J., Franzen R., Ngyuen T.,
Salamini F., Rohde W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes.";
Plant Mol. Biol.
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01-MAR-2002 (TrEMBLrel.
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InterPro; IPR002100; TF_MADSbox.
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                                                                                    LysValGluThrIleGlnLysCysGlnLys
                                                                                                                                                                                               TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT
                                                                                                                                                                                                                                    AlaGluValGlyLeuIleIlePheSerThrLysGlyLysLeuTyrGluPheSerThrGlu
                                                                                                                                                                                                                                                                                    PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGluIleSerValLeuTyrAsp
                                                                                                                                                                                                                                                                                                                                   MetGlyArgArgLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr
                                                                                                          AAGATTGAGACCATACAAAAATGTCACAAG
                                                                                                                                                            ATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCG
                                                                                                                                                                                  SerCysMetAspLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluLysValLeu
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Viridiplantae;
 (TrEMBLrel. (TrEMBLrel.
                                      PRELIMINARY;
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484.00
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yta; Liliopsida;
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4732EEBD28153879 CRC64;
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a; Poales; Poaceae; Pooidea;
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InterPro; IPR002100; TF_MADSbox.
Pfam; PF001486; K-box; 1.
Pfam; PF00319; SRF-TF: 1
PR.INTS; PR00404; MADSDOMAIN.
SMART; SM00432, MADS; 1.
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PROSITE; PS50066; MADS_BOX_2;
DNA-binding; Nuclear protein;
SEQUENCE 243 AA; 27925 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Elo A., Lemmetyinen J., Turunen M.L., Tikka L.,.Sopanen T. "Three MADS box genes homologous to SQUAMOSA and APETALA1 different expression patterns in silver birch (Betula pend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids I; Fagales; Betulaceae; Betula.
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MADS3.
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LysValGluLeuLeuGlnArgAsnHisArg
                                                                                              ValAlaAlaAspSerGluGlyGlnGlySerTrpThrMetGluPheAlaArgLeuLysGly
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; Transcription :
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Conservative:
Mismatches:
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RESULT 13
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DT 01-MC
DT 01-MADS
GN TAMA
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A Jia H., Cong B., Shao J., Sun C.;

A Jia H., Cong B., Shao J., Sun C.;

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

C -i- SUBMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION

R EMBL; AF139664; AAF66997.2; -.

R HSSP; P11831; 1SRS.

R InterPro; IPR002487; TF Kbox.

InterPro; IPR002487; TF MADSbox.

InterPro; IPR002100; TF_MADSbox.

Pfam; PF01486; K-box; 1.

R Pfam; PF01486; K-box; 1.

R Pfam; PF00149; SRF-TF; 1.

R Pfam; PR00404; MADSDOMAIN.

R PNART; SM00432; MADS; 1.
                             O82128 PRELIMINARY;
O82128;
O1-NOV-1998 (TrEMBLrel. 08, C
01-NOV-1998 (TrEMBLrel. 20, L
01-MAR-2002 (TrEMBLrel. 20, L
MADS box transcription factor
       MADS box t
TAMADS#11.
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01-MAR-2001 (TrEMBLrel:
01-MAR-2002 (TrEMBLrel:
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PROSITE; PS50066; MADS_BOX_2;
DNA-binding; Nuclear protein;
SEQUENCE 246 AA; 28394 MW;
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HSSP, P11746; 1MNM.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF001486; K-box; 1.
Pfam; PF00149; SRF-TF; 1.
Pfam; PF00179; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SWART; SM00432; MADS; 1.
Q9LEI2
Q9LEI2;
01-OCT-2000
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PROSITE; PS50066; MADS_BOX_2;
DNA-binding; Nuclear procein;
SEQUENCE 244 AA; 27718 MW;
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SEQUENCE FROM
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C STRAIN-GERES;
C STRAIN-GERES;
A Gocal G.F.W., Blundell C., Schwartz O.M., King R.W.;
T "Expression of Two APETALA1-Related Genes Changes During Infloi Initiation of Lolium.";
Initiation of Lolium.";
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
C --- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
C --- SUBLILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTOR EMBL; AF035378; AAD10625.1; ---
DK HISSP; P11831; 1SRS.
R HISSP; P11831; 1SRS.
R InterPro; IPR002100; TF MADSDox.
Pfam; PF01486; K-box; 1.
R Ffam; PF01486; K-box; 1.
R Ffam; PF03119; SRF-TF; 1.
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SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS BOX 1; 1
PROSITE; PS50066; MADS BOX 2; 1
DNA-binding; Nuclear protein; T
SEQUENCE 245 AA; 28039 MW;
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                                                   ATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCG
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Q9SEX0;
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Gryza sativa (Rice).

Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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Pfam; PF00319; SRF-TF; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
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InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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plant Physiol. 120:1193-1204(1999)
EMBL; AF058697; AAF19047.1; -.
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Moon Y.H., Kang H.G., Jung J.Y., Jeon J.S., Sung S.K., An G.;
Moon Y.H., Kang the motif responsible for interaction between the "Determination of the motif responsible for interaction between the rice APETALA1/AGAMOUS-LIKE9 family proteins using a yeast two-hybrid
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PS50066; MADS_BOX_2;
246 AA; 28523 MW;
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"MADS box genes expressed in developing inflorescences of ric

"Sorghum.";

Mol. Gen. Genet. 253:615-623(1997).

EMBL; U32110; AAB50181.1; -.

R HSSP; P11831; 1SRS.

R HSSP; P11831; 1SRS.

R TRANSFAC; T03172; -.

R InterPro; IPR002407; TF Kbox.

R InterPro; IPR002100; TF_MADSbox.

R InterPro; IPR002100; TF_MADSbox.

R Pfam; PF01486; K-box; 1.

R Pfam; PF01486; K-box; 1.

R Pfam; PF00149; SRF-TF; 1.

R PFAM; PF00319; SRF-TF; 1.

R PRINTG; PR00404; MADSDOWAIN.

R PROSITE; PS00066; MADS BOX 2; 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Panicoideae; Andropogoneae; Sorghum.
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MEDLINE=97218034; PubMed=9065695;
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Kyozuka J., Kobayashi T., Morita M., Shimamoto K.;

"Spatially and temporally regulated expression of rice MADS bo
"in the similarity to Arabidopsis class A, B, C genes.";

"plant Cell physiol 0.0-0(2000).

"in the similarity: To THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACE

"in SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACE

"Interpro; IPR002487; TF Kbox.

"Interpro; IPR002487; TF Kbox.

"Interpro; IPR002100; TF MADSbox.

"R Interpro; IPR002100; TF MADSbox.

"R Pfam; PF01486; K-box; 1.

"R Pfam; PF01486; K-box; 1.

"R Pfam; PF01496; MADS-BOX 1.

"R PFAMITS; PR00404; MADS-BOX 1; 1.

"R PROSITE; PS00350; MADS-BOX 1; 1.
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01-MAR-2002 (TrEMBLrel.
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                                                                                                                                                                             PRINTS; PRO0404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1
PROSITE; PS50066; MADS_BOX_2; 1
DNA-binding; Nuclear protein; T
SEQUENCE 270 AA; 31039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Heuer S., Hansen S., Bantin J., Brettschneider R., Kranz Dresselhaus T.;
"The maize WADS box gene ZmMADS3 affects node number and development and is co-expressed with ZmMADS1 during flowe development, in egg cells, and early embryogenesis."; elart Physiol 127:33-45(2001).

-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-SUMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTIO EMBL; API12150; AAG43200.1; -.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2002 (TrEMBLrel. 20,
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InterPro; IPR002100; TF MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
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STRAIN=A188;
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Transcription regulation.
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Length:
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Oryza sativa (Rice).
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Gao Z. Chen R., Jia H., Sun C.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ da
EMBL; AR345911; AA109473.1; -
InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF_MADSbox.
InterPro; PR003100; TF_MADSbox.
Pfam; PF00319; SRF-TF; 1.
Pfam; PF00319; SRF-TF; 1.
PROSITE; PS500366; MADS BOX 2; 1.
SEQUENCE 267 AA; 31266 MW; 1003B3419DED35CD
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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                                                   TTCTCCAAGCGCCCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGAC
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                                 InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF MADSbox.
Pfam; PF001486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
PR.NTS; PR00404; MADSDMAIN.
SMART; SM00432; MADS; 1.
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PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS BOX 1; 1
PROSITE; PS50066; MADS BOX 2; 1
DNA-binding; Nuclear protein; T
SEQUENCE 273 AA; 31248 MW;
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01-NOV-1999 (TrEMBLrel. 12, 1
01-MAR-2002 (TrEMBLrel. 20, 1
MADS box-like protein.
Oryza sativa (Rice).
                                                                                                                                        STRAIN-CV. NIPPONBARE; TISSUE-PANICLE AT PRE-MEIOTIC STANSHIOLOGUEA Y., Yamamoto K., Sasaki T.;
"Characterization of rice MADS box-like genes.";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003325; BAA81883.1; -.
HSSP; P11831; 1SRS.
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PF00319;
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PS50066; MADS_BOX_2; 1.
267 AA; 30391 MW; 5A31330C64180D92
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SRF-TF; 1
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01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                              MEDLINE=99373407; PubMed=10444103; Moon J.S., Sung S.K., An G.; Moon Y.H., Kang H.G., Jung J.Y., Jeon J.S., Sung S.K., An G.; "Determination of the motif responsible for interaction between rice APETALAI/AGAMOUS-LIKES family proteins using a yeast two-hypersex.";
                                                                                     PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS50066; MADS_BOX_2
SEQUENCE 267 AA; 30415 MW
                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                          Pfam; PF01486; K-box; 1. Pfam; PF00319; SRF-TF; 1.
                                                                                                                                                                                           Plant Physiol. 120:1193-1204(1999)
EMBL; AF058698; AAF19048.1; -.
HSSP; P11831; 1SRS.
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=FLOWER;
                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
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4.85e-42
557.00
98.18%
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80B1770C60584ABF
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                                     Length:
Matches:
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Matches:
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st Local Similarity:
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y Match:
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01-MAY-1999
01-MAY-1999
01-MAR-2002
SEQUENCE FROM N.A.

STRAIN-CERES;
Gocal G.F.W., Blundell C., Schwartz O.M., King R.W.;
Gocal G.F.W., Blundell C., Schwartz O.M., King R.W.;
"Expression of Two APETALA1-Related Genes Changes During
Initiation of Lolium.";
Subfilted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELTULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTI-
EMBL; AF035379; AAD10626.1; -.
                                                                                                                             Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
Poeae; Lolium.
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PROSITE; PS50066; MADS_BOX_2;
DNA-binding; Nuclear protein;
SEQUENCE 276 AA; 31839 MW;
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PRINTS; PR01574; TUBBYPROTEIN.
SMART; SM00432; MADS; 1.
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InterPro; IPR002487; TF Kbox.
InterPro; IPR00210; TF MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF00319; SRF-TF; 1.
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/ta; Liliopsida; Poales; Poaceae;
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Matches:
Conservative:
Mismatches:
Indels:
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InterPro; IPR002487; TF Kbox.
InterPro; IPR002100; TF MADSbox.
InterPro; IPR002100; T MADSbox.
Pfam; PF01486; K-box; 1.
Pfam; PF001486; K-box; 1.
PFRNTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
SMART; SM00432; MADS; 10.
PROSITE; PS000350; MADS BOX 1; 1.
PROSITE; PS000350; MADS BOX 2; 2.
DNA-binding; Nuclear Protein; Tran
SEQUENCE 261 AA; 30025 MW; 176
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01-NOV-1996
01-MAR-2002
                                                                                                                                                                                                                                                                                           Zea mays (Maize).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q41829
Q41829;
  EMBL; L46400; AAB00081.1;
HSSP; P11831; 1SRS.
InterPro; IPR002487; TF_K
InterPro; IPR002100; TF_M
                                                                                                                              SEQUENCE FROM N.A.
TISSUE=FEMALE INFLORESCENCE;
TISSUE=9613214; PubMed=8580958;
MEDLINE=9613214; PubMed=70.R., Mena M., Mandel M.A., Lerner D.R., Mena M., Mena 
                                                                                                                                                                                                                                                                                                                                                                                                                 MADS
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NCBI_TaxID=4577;
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                                                                                     SUBCELLULAR LOCATION: NUCLEAR SIMILARITY: TO THE MADS DOMAII
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TF_Kbox.
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-Q=/cgn2 1/USPTO_spool/US10020338/runat_24062003_102354_21507/app_query.fasta_1.775
-Q=/cgn2 1/USPTO_spool/US10020338/runat_24062003_102354_21507/app_query.fasta_1.775
-DS-SPTREMBL_21 -QFMT=fastan -SUFFIX=rSpt -MINMATCH=0.1 -LOOPCL=0 -LOOPCXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi .IJST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10020338_GCGN_1 1_138_grunat_24062003_102354_21507 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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genes."; Plant Mol. Biol. 42:899-913(2000)i- SUBCELLULAR LOCATION: NUCLEAR -i- SIMILARITY: TO THE MADS DOMAIN	Franzen R., Ngyu Rohde W.; pping and expres	STRAIN=CV. ATLAS; TISSUE=FLOWER; MEDLINE=20146590: DubMed=10890536:	M N.A.	513;	ordeum.	a; Magnoliophyta	'iridiplantae; St	Hordeum vulgare (Barley).	ינפדון ס.	01-JUN-2002 (TremBire). 21, Last annotation update)	(TrEMBLrel. 15,	(TrEMBLrel. 15,		PRELIMINARY;	-	
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genes."; Plant Mol. Biol. 42:899-913(2000). -i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY) -i- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.	Schmitz J., Franzen R., Ngyuen T., Garcia-Maroto F., Pozzi C., Salamini F., Rohde W.; "Cloning, mapping and expression analysis of six barley MADS-box					Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	•		n update)	update)			Α.		

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-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE
-!- SUBCELLULAR LOCATION: NUCLEAR (By Similarity).

-!- SUBCELLULAR LOCATION: NUCLEAR (By Similarity).

-!- TISSUE SPECIFICITY: EXPRESSED IN PETALS AND WEAKLY IN SEPALS BUT
NOT IN THE COLUMN (GYNOSTEWIUM).

-!- DEVELOPMENTAL STAGE: EXPRESSED IN MATURE FLOWERS AND NOT IN YOUNG
DEVELOPING INFLORESCENCES OR YOUNG FLORAL BUDS.

-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                           the European Bioinformatics Institute. Thuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=94072738; PubMed=8251643;
Lu Z.X., Wu M., Loh C.S., Yeong C.Y., Goh C.J.;
"Nucleotide sequence of a flower-specific MADS orchid.";
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS BOX 1;
PROSITE; PS50066; MADS_BOX_2;
                                                            InterPro; IPR002487; TF Kbox.
InterPro; IPR002110; TF MADSbox.
Pfam; PF00319; SRF-TF; T.
Pfam; PF01486; K-box; 1.
                                                                                                                                     EMBL; X69107; CAA48859.1;
HSSP; P11746; 1MNM.
                                                                                                                                                                                              modified and this statement is not removed entities requires a license agreement (See
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between the Swiss Institute of Bioinformatics and the EMBL
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15-JUN-2002 (Rel. 41,
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                                                                                                                                                                                equires a license agreement (S email to license@isb-sib.ch).
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DOMAIN 96 168 K-BOX.
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                                                                                                                                TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCT-----
                                                                                                                                                                                                                                                                                ATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACC
AAGGCGAAGATTGAGACCATACAAAAATGTCACAAG
                                                    ThrIleIleSerArgGluThrGlnSerSerGln-----
                                                                             GCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTT
                                                                                                       ThrSerMetLeuLysThrLeuGluLysTyrGlnLysCysAsnPheGlySerProGluSer
                                                                                                                                                         AlaGluValAlaLeuIleIlePheSerAsnArgGlyLysLeuTyrGluPheCysSerSer
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                                                                                                                                                                                                              PheAlaLysArgArgLysArgLeuLeuLysLysAlaTyrGluLeuSerValLeuCysAsp
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Search completed: June 24, 2003, 14:12:49 Job time : 16 secs

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RESULT 14
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ID AGL9
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                                                                                                                                    AGL9 ARATH STANDARD; FRAL, O22456;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16 Agamous-like MADS box protein AGL9.
17 AGL9 OR ATIG24260 OR F316.19
18 Arabidopsis thaliana (Mouse-ear cress)
18 Arabidopsis thaliana Streptophyta; Embryophyta; Embryophyta; Viridiplantae; Streptophyta; Embryophyta; Arabidopsis co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00319; SRF-TF; Pfam; PF01486; K-box; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
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PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding;
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Interpro; IPR002100; TF MADSbox.
Pfam; PF00319; SRF-TF; I.
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                                                       SEQUENCE FROM N.A
                                                                                                                                 Spermatophyta; Magnoliophyta;
eurosids II; Brassicales; Bras
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                             Landsberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 AA;
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29603 MW;
                                                                                                                              Brassicaceae;
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63
23
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263

ATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACC

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STTREET DESCRIPTION OF THE STREET OF THE STR
US-10-020-338-8 (1-593) x AGL9_ARATH (1-251)
                                                                                                                    Best Local Similarity:
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                                                                                          Query Match:
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RX Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S., RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y., RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K., RA Chung M.K., Coun, Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y., RA Chung M.K., Chung T.V., Feng J.-D., Fong B., Fujii C.Y., RA Lin J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L., RA Minter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E., RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B., RA Langin-Hopper S., Liu Z.A., Luros J.S., Maiti R., Marziali A., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A., RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., RA Militscher J., Saltano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M., RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
Thaliana ", Fraser C.M., Venter J.C., Davis R.W.;
Thaliana ", Angle G. G. G. Connosome 1 of the plant Arabidopsis RT Tallon L.G. G. (2007)
                                                                                                                                                                                                                                                                                                                                                                                                                   R InterPro; IV3032; -.

R InterPro; IPR002487; TF Kbox.

R InterPro; IPR002100; TF MADSbox.

Pfam; pF00319; SRF-TF; I.

PFINTS; PR00404; MADSDOMAIN.

SMART; SM00432; MADS; 1.

PROSITE; PS00350; MADS_BOX_1; 1.

PROSITE; PS00366; MADS_BOX_1; 1.
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Sex. Plant Reprod. 11:22-28(1998)
[2]
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EMBL; AC002396; AAC00586.1; -.
HSSP; P11746; 1MNM.
TRANSFAC; T03032; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                      Transcription
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SUBCELLULAR LOCATION: Nuclear (By similarity)
DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING F
WITHIN PETALS, STAMENS, AND CARPELS.
SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY
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PS50066; MADS_BOX_2; 1.
PS50066; MADS_BOX_2; 1.
Ption regulation; DNA-binding; Nuclear
MADS.
3 7 MADS.
                                                                                                                                                                                                                                                                                                            251 AA;
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53.85%
30.53%
                                                                                                                                                                                                                                                                                                            29066 MW;
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                                                                                                                                                                                                                                                                                                                                         K-BOX
                                                                                                                                                                                                                                                                                                               0057CABD3F1AFC40 CRC64;
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Matches:
Conservative:
Mismatches:
                                                          Gaps:
                                                                                          Indels:
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RESULT 12
AGL9_LYCE:
CREAL AND SOUCH DESCRIPTION OF THE STATE OF 
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              Pfam; PF00319; SRF-TF; Pfam; PF01486; K-box; 1
PRINTS; PR00404.
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STRAIN=cv. VENT Cherry; TISSUE=Flower;
MEDLINE=93251098; PubMed=1688249;
Pnuell L., Abu-Abeid M., Zamir D., Nacken W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-DEC-1998
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15-JUN-2002
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Q42464;
                                                                                                                                                                                                                                        EMBL; X60758; CAA43170.1; -.
EMBL; X60480; CAA43010.1; -.
HSSP; P11746; IMNM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
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Lycopersicon escuteur
                                                                                                                                                                                                                                                                                                                                                                                     or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                      InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lifschitz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agamous-like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE IN INFLORESCENCE DEVELOPMENT AND FLORAL ORGANOGENESIS (BY SIMILARITY).
SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: FLOWER-SPECIFIC.
SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ew
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                                                                                                                                                                                                                                                                                                                                                                                 equires a license agreement (Seemail to license@isb-sib.ch).
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  (See http://www.isb-sib.ch/announce/
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                                                                                                          function of the gene:
                                                                                                                                                                               NCBI_TaxID=3728;
                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids II; Brassicales; Brassicaceae; Sinapis.
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                                                                                                                    Bonhomme F., Sommer H., Bernier G., Jacqmard A., "Characterization of SaMADS D from Sinapis alba
                                                                                                                                          MEDLINE=97390682; PubMed=9247539;
                                                                                                                                                     TISSUE=Flower,
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                         Sinapis alba
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15-JUN-2002
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                                               FUNCTION: PROBABLE TRANSCRIPTION FACTOR ACTIVE DEVELOPMENT AND FLORAL ORGANOGENESIS.
SUBCELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY C
                              SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
SWISS-PROT entry is copyright.
een the Swiss Institute of Bio
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OX_2; 1.
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ery Match:
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P29384;
01-DEC-1992 (Rel.
01-DEC-1992 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                    01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-UN-2002 (Rel. 41, Last sanotation update)
15-UN-2002 (Rel. 41, Last annotation update)
Agamous-like MADS box protein AGL4.
AGL4 OR AT3G02310 OR F14P3.4.
ARGL4 OR AT3G02310 OR F14P3.4.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosid.
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DOMAIN
SEQUENCE
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Pfam; PF01486; K-box; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                   Ma H., Yanoi
"AGL1-AGL6,
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PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding;
                                                                                           SEQUENCE FROM N.A.
MEDLINE=91160981; PubMed=1672119;
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  MEDLINE=21016720;
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                                             Yanofsky M.F., Meyerowitz E.M.;
AGL6, an Arabidopsis gene family with
ic and transcription factor genes.";
Dev. 5:484-495(1991).
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| SerAsnMetLeuLysThrLeuAspArgTyrGlnLysCysSerTyrGlySerTleGluVal
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248 AA;
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US-10-020-338-8 (1-593) x AGL4_ARATH (1-250)
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Fartmann B., Valle G., B.
Fartmann M., Boutry M., G.
Choisne N
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                                                                                                                                                                                                                                                      PROSITE; PS00350; MADS_BOX 1; 1.
PROSITE; PS50066; MADS_BOX 2; 1.
Transcription regulation; DNA-binding; Nuclear DOMALN 3 57 MADS.
DOMALN 97 169 K-BOX.
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Pfam; PF01486; K-box; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib-
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-!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- DEVELOPMENTAL STAGE: EXPRESSED EARLY DURING FLOWER DEVELOPMENT.
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                       SEQUENCE
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InterPro; IPR002100; TF MADSbox.
Pfam; PF00319; SRF-TF; 1.
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
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                                                  Brottier P.,
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Shea T.P.,
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                   Angenent G.C.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ data
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ data
-i- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-i- SUBCELLULAR LOCATION: Nuclear.
-i- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                             PRINTS; PR00404; MADSDOMAIN. SMART; SM00432; MADS; 1.
                                                                                                        InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF00319; SRF-TF; I.
Pfam; PF01486; K-box; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93005737; PubMed=1356537; Angenent G.C., Busscher M., Franken "Differential expression of two MADS mutant petunia flowers."; Plant Cell 4:983-993(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Petunia hybrida (Petunia).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 SEQUENCE
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                                                    PS50066; MADS_BOX_2;
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                      regulation; DNA-binding;
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Last annotation update)
protein AGL9 homolog (F
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y Match:
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entities
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         EMBL; M55551; AAA32732.1; PIR; B39534; B39534.
                                                                            use
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                                                                                                             This
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                                                     Buropean Bioinformatics Institute. There by non-profit institutions as long as fitied and this statement is not removed. It is requires a license agreement (See htt
                                                                                                                                    SIMILARITY: CONTAINS 1 K-BOX DIMERIZATION DOMAIN.
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EMBL; AF386929; AAK62374.1; -.
EMBL; AY072463; AAL66878.1; -.
HSSP; P11746; 1MNM.
TRANSFAC; T03030; -.
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Gu Q., Ferrandiz C., Yanofsky M.F., Martier
"The FRUITFULL MADS-box gene mediates cell
Arabidopsis fruit development.";
Development 125:1509-1517(1998).
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STRAIN=cv.
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PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNa-binding;
DOMAIN 3 57 MADS.
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Pfam; PF01486; K-box; 1
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SUBCELLULAR LOCATION: Nuclear (By similarity).
TISSUE SPECIFICITY: Vascular tissue of cauline leaves, fl
shoot apex and valves of carpels and fruits.
INDUCTION: Dramatically up-regulated upon the transition
vegetative to reproductive development.
SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRI
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                                                                          TTCTCCAAGCGCCCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGAC
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                                                                                                                                                                                                 ATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACC
ATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCG
                                                                                                                              PheSerLysArgArgSerGlyLeuLeuLysLysAlaHisGluIleSerValLeuCysAsp
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IPR002100; TF_MADSbox.
)0319; SRF-TF; 1.
                     TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAAGGCTCTT
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; 27536 MW;
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                                                                                                                                                                                                                                                                                                                                                                                  K-BOX
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es cell differentiation
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HSSP; P11746; IMNM.
TRANSFAC; T03060; -
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002187; TF_MADSbox.
Pfam; PF00319; SRF-TF; I.
Pfam; PF01486; K-box; 1.
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DOMAIN
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00350; MADS BOX 1; 1.
PROSITE; PS50066; MADS BOX 2; 1.
Transcription regulation; DNA-binding;
DOMAIN
3 58 MADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a convergent the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=cv: Scania; TISSUE=Petal;
Baudinette S.C., Savin K.W.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRJ
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15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUN-2002 (Rel. 41,
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                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sinapis alba (White mustard) (Brassica hirta).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Sinapis.
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Q41274;
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                                                                                                                      PRINTS; PR00404; MADSDOMAIN. SMART; SM00432; MADS; 1.
                                                                                                                                             InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF00319; SRF-TF; 1.
Pfam; PF01486; K-box; 1.
                                                                                                                                                                                                         EMBL; U25695;
HSSP; P11746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97077349; PubMed=8919916;
Menzel G., Apel K., Melzer S.;
"Identification of two MADS box genes that are expressed in the
apical meristem of the long-day plant Sinapis alba in transition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998
15-DEC-1998
15-JUN-2002
                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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             No.:
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SUBCELLULAR LOCATION: Nuclear (By similarity).
DEVELOPMENTAL STAGE: EXPRESSED IN APICAL MERISTEMS
                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. There are no
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                          Scores:
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                                                                                 PS00350; MADS_BOX_1; 1.
PS50066; MADS_BOX_2; 1.
ption_regulation; DNA-binding;
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Best Local Similarity:
                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=98162728; Pub
Nakamura Y., Sato S.,
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
"RIKEN Arabidopsis full length cDNA clones (RAFLs) sequer
"RIKEN Arabidopsis full length CDNA clones (RAFLs) sequer
SSP consortium (Salk/Stanford/PGEC).";
SSP consortium (Salk/Stanford/PGEC).";
                                                                                                                                                                                                                                                                                                                                                                                                                            Q38876;
15-DEC-1998
15-DEC-1998
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARATH
AGL8_/
                                                                                                        "Structural analysis of Arabidopsis thaliana of Sequence features of the regions of 1,191,918 physically assigned Pl clones.";
DNA Res. 4:401-414(1997).
                                                                                                                                                                                                                                Wandel M.A., Yanofsky M.F.;
"The Arabidopsis AGL8 MADS box gene meristems and is negatively regulate plant Cell 7:1763-1771(1995).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=96093419; PubMed=8535133;
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Arabidopsis thaliana (Mou
                                                                                                                                                                                                                                                                                                                                                                                                     Agamous-like (FRUITFULL).
                                                                                                                                                           Tabata S.;
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S., Kaneko T.,
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SEQUENCE
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InterPro; IPR002100; TF_MADSbox.
Pfam; PF00319; SRF-TF; T.
Pfam; PF01486; K-box; 1.
PRINTS; PR00404; MADSDOMAIN.
SMART; SM00432; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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STRAIN=CV. VFNT Cherry; TISSUE=Flo
MEDLINE=92251098; PubMed=1688249;
Pnueli L., Abu-Abeid M., Zamir D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding;
DOMAIN 3 57 MADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
-i- SUBCELLULAR LOCATION: Nuclear (By similarity).
-i- TISSUE SPECIFICITY: FLOWER-SPECIFIC.
-i- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The MADS box gene family in tomato: temporal expression during floral development, conserved secondary structures and homology homeotic genes from Antirrhinum and Arabidopsis."; Plant J. 1:255-266(1991).
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[1]
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EMBL; U23757; AAA92839.1; -.
HSSP; P11746; 1MNM.
TRANSPAC; T03145; -.
InterPro; IPR002487; TF_Kbox.
InterPro; IPR002100; TF_MADSbox.
Pfam; PF00319; SRP-TF; 1.
Pfam; PF001486; K-box; 1.
PRINTS; PR00404; MADSSOMAIN.
SMART; SM00432; MADS; 1.
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15-DEC-1998 (Rel. 3
15-JUN-2002 (Rel. 4
Agamous-like MADS k
Solanum tuberosum
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PROSITE; PS50066; MADS_BOX 2; 1.
Transcription regulation; DNA-Inding; Nuclear DOMAIN 3 57 MADS.
DOMAIN 3 57 K-BOX.
SEQUENCE 250 AA; 28922 MW; EDE37FFFE793DDC4
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STRAIN=cv. Superior;
MEDLINE=96343939; PubMed=8756601;
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum
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101 ArgLeuGluValLeuGlnArgAsnGlnLys
                                                                         TTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCCGTCCTCTGTGAC 382
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Seppanen M.M.;

Seppanen M.M.;

Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.

-i- SUBCELLULAR LOCATION: Nuclear (By Similarity).

-i- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRA
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                                                                                                                                             Floral homeotic protein APETALA1 (AGL7 protein).
API OR AGL7 OR AT1G69120 OR F4N2.9.
API OR AGL7 OR AT1G69120 OR F4N2.9.
Arabidopsis thaliana (Mouse-ear Cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                AP1 ARATH STANDARD; PRT; 256 AA. P35631; Q9LQA8; O1-JUN-1994 (Rel. 29, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
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SEQUENCE
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SMART; SM00432; MADS; 1.
PROSITE; PS00350; MADS_BOX_1; 1.
PROSITE; PS50066; MADS_BOX_2; 1.
Transcription regulation; DNA-binding;
                                                                    STRAIN=cv. Landsberg erecta;
MEDLINE=93063372; PubMed=1359429;
Mandel M.A., Gustafson-Brown C.,
                                                                                                                             eurosids II; Brassicales;
NCBI_TaxID=3702;
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Pfam; PF01486; K-box; 1.
SEQUENCE FROM N.A. STRAIN=cv. Columbi
                                                          Mandel M.A., Gustafson-Brown "Molecular characterization
                                   Nature 360:273-277(1992)
                                                                                               STRAIN=cv.
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InterPro; IPR002100; TF_MADSbox
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Couway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Couway A.R., Creasy T.H., Dewar K.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Liam B.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Liam B.,
RA Langin-Hooper S., Lee A., Lucos J.S., Maiti R., Marziali A.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Riyuyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chrömosome 1 of the plant Arabidopsis
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Genetics 160:1641-1650(2002).

Genetics 160:1641-1650(2002).

-!- FUNCTION: CONTROLS FLORAL MERISTEM IDENTITY. IS ALSO RE NORMAL DEVELOPMENT OF SEPALS AND PETALS. IS REQUIRED FO TRANSITION OF AN INFLUORESCENCE MERISTEM INTO A FLORAL
between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Nuclear.
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-Q=/GGM2_1/USPTO_Spool/USI0020338/runat_24062003_102354_21495/app_query.fasta_1.775
-DB=SwissProt_40 -QFMT=fastan -SUFFIX=rSp -MINVATCH=0.1 -LOOPCH=0 -LOOPEXT=0
-UNITS=bits -START=1 = END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-USER=US10020338_@CGN 1 1 26 @runat 24062003 102354 21495 -NCPU-6 -ICPU=3
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;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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'Cross-references: EMBL:Y15008; PIDN:CAA75241.1
Experimental source: subsp. Japonica, cv. Zhonghua 8, flower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bmitted to the EMBL Data Library, September 1997
Reference number: Z15271
Accession: T04307
Status: preliminary; translated from GB/EMBL/DDBJ
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Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
Accession: T04307
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                                    557 AAGGCGAAGATTGAGACCATACAAAAATGTCACAAG 592
                                                                                                              497 GCTCTTATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTT 556
                                                                                                                                                                      443 TCCAGCATGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCT-----GAAAAG 496
                                                                                                                                                                                                                                                                                                                     323 TTCTCCAAGCGCCGCAACGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGAC 382
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LysAlaArgValGluAsnLeuGlnArgThrGlnArg 112
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Search completed: June 24, 2003, 14:10:34

Job time : 27 secs

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A;Cross-references: EMBL:X80902; NJ
A;Accession: S51935
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 92-156 <TA2>
C;Genetics:
C;Genetics:
A;Gene: dall
C;Superfamily: transcription factor
C;Keywords: DNA binding; transcript
F;2-57/Domain: serum response factor
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A;Description: Carnation MADS box genes.
A;Reference number: Z17094
A;Accession: T10714
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-233 cBAU>
A;Experimental source: Cv. Scania; petals
C;Genetics:
                                                                                                                                                                                                                                              probable MADS-box protein dall - Norway spruce C;Species: Picea abies (Norway spruce) C;Date: 14-Jul-1995 #sequence_revision 01-Dec-2000 #text_C;Accession: T14846; S51935 R;Tandre, K.; Albert, V.A.; Sundas, A.; Engstroem, P. Plant Mol. Biol. 27, 69-78, 1995 Plant Mol. Biol. 27, 69-78, 1995 A;Title: Conifer homologues to genes that control floral A;Reference number: S51934; MUID:95170009; PMID:7865797 A;Accession: T14846
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C;Superfamily: transcription factor squa; serum response factor DNA-binding C;Keywords: DNA binding; transcription factor; transcription regulation C;Keywords: DNA binding; transcription factor; transcription regulation F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
                                                                                                                                                                                          A;Status: preliminary; translated
A;Molecule type: mRNA
A;Residues: 1-261 <TAN>
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LysValAspValLeuGlnArgSerHisArg 109
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A binding; transcription regulation
serum response factor DNA-binding domain homology <SRF>
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                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A;Reference number: Z16765
A;Accession: T09603
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C;Species: Pinus radiata (Monterey pine)
C;Date: 16-Jul-1999 #sequence_revision 1
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A;Experimental source: tissue-type immature male and female
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A; Residues: 1-261 < MOU>
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R; Kempin, S.A.; Savidge, B.; Yanofsky, M.F. Science 267, 522-525, 1995
A;Title: Molecular basis of the cauliflower A;Reference number: Z18101; MUID:95125463; P A;Accession: T14457
A;Status: preliminary; translated from GB/EM A;Molecule type: mRNA A;Residues: 1-150 KEM5
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                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADS box protein homolog CAL - broccoli
;Species: Brassica oleracea var. botrytis (broccoli)
;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t
                                                                                                                                                                                                                                                                       gnment Scores:
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                                    AlaGluValSerLeuIleValPheSerHisLysGlyLysLeuPheGluTyrSerSerGlu
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             TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT
                                                            GCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCACCGAC 442
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MADS-box protein CMB1 - clove pink C;Species: Dianthus caryophyllus (clove C;Date: 16-Jul-1999 #sequence_revision C;Accession: T10714 R;Baudinette, S.C.; Savin, K.W.
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Science 267, 522-525,
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C;Superfamily: transcription factor squa; serum response factor DNA-binding C;Keywords: DNA binding; nucleus; transcription regulation F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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A;Experimental source: floral meristem
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LysAlaLysIleGluLeuLeuGluArg
                                    AAGGCGAAGATTGAGACCATACAAAAA
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homo

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e pink) 16-Jul-1999

#text_change 21-Jan-2000

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A;Gene: 'TUK'
A;Map position: 6
A;Map position: 6
C;Superfamily: transcription factor squa; serum response factor DNA-binding
C;Keywords: DNA binding; nucleus; transcription regulation
C;Keywords: DNA binding; nucleus; transcription domain homology <SRF>
F;2-57/Domain: serum response factor DNA-binding domain homology <SRF>
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M;Alternate names: Eforal homeotic protein TM4
C;Species: Lycopersicon esculentum (comato)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 24-Sep-1999
C;Accession: S23730
R;Pnueli, L; Abu-Abeid, M.; Zamir, D.; Nacken, W.; Schwarz-Sommer, Z.; Lifschi Plant J. 1, 255-266, 1991
A;Title: The MADS box gene family in tomato: temporal expression during floral A;Accession: S23728; MUID:93251098; PMID:1688249
A;Accession: S23730
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                A;Title: Nucleotide sequences of novel potato A;Reference number: Z15919; MUID:96125213; PM. A;Accession: T07100
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Residues: 1-227 < PNU>
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F; 2-57/Domain: s
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A; Residues: 1-242 < MAN>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28 Oct-1996 #sequence_revision 27-Feb-1997
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A; Residues: 1-250 «KANS
A; Cross-references: EMBL:U23757; NID:9758564; PIDN:AAA92839.1; PID:9758565
A; Experimental source: cv. Superior; vegetative tissue; tuber induced 4-day
C; Genetics:
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dbmitted to the EMBL Data Library, October 1992
A;Reference number: $36597
A;Accession: $36597
A;Accession: $36597
A;Rolecule type: mRNA
A;Residues: 1-235,237-256 </ANN
A;Cross-references: EMBL:216421; NID:g16161; PIDN:CAA78909.1;
C;Genetics:
A;Map position: 1
C;Superfamily: transcription factor squa; serum response factor C;Keywords: DNA binding; nucleus; transcription regulation
F;2-57/Domain: serum response factor DNA-binding domain homolo
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827109
MADS box protein AP1 - Arabidopsis thaliana
NALternate names: floral homeotic protein AP1
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-C;Accession: 827109; 836597
R;Mandel, M.A.; Gustafson-Brown, C.; Savidge, B.; Yanofsky, M.F.
Nature 360, 273-277, 1992
A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the Arabidopsis floral homeotic in A;Title: Molecular characterization of the A;Title: Molecular characterization of
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A; Residues: 1-256 < MAN>
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C;Species: Solanum commersonii (Commerson's wild potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change
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Best Local Similarity:
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A; Residues: 1-250 < SEP>
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                       ATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCG
                                                                              SerCysMetGluArgLeuLeuGluArgTyrGluArgTyrSerPheAlaGluLysGlnLeu
                                                                                                      TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT
                                                                                                                                                                   AlaGluValGlyLeuIleValPheSerThrLysGlyLysLeuPheGluTyrAlaThrAsp
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Mol. Gen. Genet. 253, 615-623, 1997
A, Title: MADS box genes expressed in developing inflorescences A, Fittle: MADS box genes expressed in developing inflorescences A, Facesesion: T14737
A, Accession: T14737
A, Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A, Residues: 1-228 <GRE>
A, Cross-references: EMBL:U32110; NID:g1905933; PIDN:AAB50181.1; C; Gene: MADS2
C; Superfamily: transcription factor squa; serum response factor C; Keywords: DNA binding; nucleus; transcription regulation
RESULT 3
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Best Local Similarity:
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pecies: Sorghum bicclor (sorghum)
Date: 20-Sep-1999 #sequence_revision
Accession: T14737
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                                                                                                             SerGluSerGluGlyAsnTrpCysHisGluTyrArgLysLeuLysAlaLysIleGluThr
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Alignment

Scores:

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MADS box protein ap1 - white mustard N;Alternate names: floral homeotic protein C;Species: Sinapis alba (white mustard) C;Date: 07-May-1995 #sequence_revision 21-J
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A;Title: Bracteomania, an inflorescence anomaly, is caused A;Reference number: $20886; MUID:92224862; PMID:1563342
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C;Species: Antirrhinum majus (garden snapdragon)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992
C;Accession: $20886
A;Cross-references: EMBL:X81480; NID:g609252; PIDN:CAA57233.1; PID:g609253 C;Superfamily: transcription factor squa; serum response factor DNA-binding C;Keywords: DNA binding; nucleus; transcription regulation C;Keywords: DNA-binding domain homology <SRF>
                                                                A; Molecule type: mRNA
A; Residues: 1-254 <MEN>
                                                                                             A; Reference number: S52236
A; Accession: S52236
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R;Menzel, G.; Apel, K.; Mel
submitted to the EMBL Data
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A; Residues: 1-248 < HUI>
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-Q=/Cgn2 1/USPTO_spool/US10020338/runat_24062003_102355_21519/app_query.fasta_1.775
-Q=/Cgn2 1/USPTO_spool/US10020338/runat_24062003_102355_21519/app_query.fasta_1.775
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-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIEN=200000000
-USER=US10020338 @CGN 1 1 62 @runat 24062003 102355_21519 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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ALIGNMENTS

Ş 밁 Ş A;Note: ZAP1 C;Superfamily: transcription factor squa; serum response factor I F;2-57/Domain: serum response factor DNA-binding domain homology DB: Percent Similarity:
Best Local Similarity:
Query Match: Alignment Scores: Pred. No.: A; Reference number: A; Accession: T03410 R;Mena, M.; Mandel, M.A.; Lerner, D.R.; Yanofsky, M.F.; Schmidt, R.J. Plant J. 8, 845-854, 1995
A;Title: A characterization of the MADS-box gene family in maize.
A;Reference number: Z14928; MUID:96132144; PMID:8580958 C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Sep-1999 C; Species: Zea mays MADS box protein - maize US-10-020-338-8 (1-593) x T03410 (1-273) Score: A; Molecule type: mRNA A; Residues: 1-273 <MEN> A; Status: preliminary; translated C; Accession: T03410 A; Cross-references: Genetics: 323 263 21 <u>, ...</u> MetGlyArgGlyLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr TTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCCGTCCTCTGTGAC ATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACC PheSerLysArgAsnGlyLeuLeuLysLysAlaHisGluIleSerValLeuCysAsp EMBL:L46400; NID:g939784; PIDN:AAB00081.1; PID:g939785 (maize) 8.9e-43 561.00 99.09% 99.09% 54.47% from GB/EMBL/DDBJ Gaps: Conservative: Mismatches: Matches: Indels: 273 109 0 . 1 0 factor DNA-binding domain <SRF> 20 40 382

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ArgTyrGluAsnLeuGlnArg 107

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US-09-853-450-32

Sequence 32, Application US/09853450

Publication No. US20020194645A1

GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 250
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                 APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: Ditta, Gary
ITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
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APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-0025400US
CURRENT APPLICATION NUMBER: US/09/853,450
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                                                                                                                                                                                                                                                                                                                                   US-10-020-338-8 (1-593) x US-09-853-450-32 (1-237)
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
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                         542 GAATACAGGAAACTTAAGGCGAAGATTGAGACCATACAAAAATGTCACAAG 592
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                                                     81 AsnValProSerArgGluAlaLeuAlaValGluLeuSerSerGln------Gln 96
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Search completed: June 24, 2003, 14:14:27 Job time: 31.5 secs

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APPLICANT: Yanofsky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of
TITLE OF INVENTION: Combinations of Genes fo
TITLE OF INVENTION: Exhibiting Modulated Re
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                             US-10-020-338-8 (1-593) x US-09-853-450-12 (1-251)
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TYPE: PRT
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APPLICANT: Ditta, Garya

APPLICANT: Ditta, Gary

APPLICANT: Ditta, Gary

APPLICANT: The Regents of the University of

ITITLE OF INVENTION: Combinations of Genes fo

ITITLE OF INVENTION: Exhibiting Modulated Re

FILE REFERENCE: 19452A-002400US

CURRENT APPLICATION UNMER: US/09/853,450

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO. 28

LENGTH: 248

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FERTURE:

FERTURE: TWEODEMATTION: CERTIFICATION (SERVICE)
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                                                                                                        Sequence 10, Application US/09853450
Publication No. US20020194645A1
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
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APPLICANT: Liljegren, Sarah
APPLICANT: Liljegren, Sarah
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in Transgenic
TITLE OF INVENTION: Plants
FILE REFERENCE: 19452A-000920US
CURRENT APPLICATION NUMBER: US/09/978,730
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR PILING DATE: 1998-06-25
PRIOR FILING DATE: 1998-06-25
PRIOR FILING DATE: 1999-06-25
          TITLE OF INVENTION:
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r: Pelaz, Soraya
r: Ditta, Gary
T: The Regents of the University of California
INVENTION: Combinations of Genes for Producing Seed Plants
INVENTION: Exhibiting Modulated Reproductive Development
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CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 255
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
  Alignment Scores: Pred. No.:
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                                                                                                                                                                                                          APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yanofsky, Martin F. APPLICANT: Pelaz, Soraya
                                                                                                                                    LENGTH: 15
TYPE: PRT
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                                                                          ORGANISM: Brassica oleracea var. FEATURE:
OTHER INFORMATION: CAULIFLOWER (
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                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yanofsky, Martin F.
APPLICANT: Liljegren, Sarah
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in
TITLE OF INVENTION: Plants
FILE REFERENCE: 1945ZA-000930US
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/99/978,382A
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/978,740A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/090,649
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: US 09/339,998
PRIOR FILING DATE: 1999-06-25
PRIOR FILING DATE: 1999-06-25
UNMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
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The Regents of the University of California
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Yanofaky, Martin F.
APPLICANT: Pelaz, Soraya
APPLICANT: Ditta, Gary
APPLICANT: The Regente of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-002400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT APPLICATION SEED IN MEMBER: US/09/853,450
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 255
Sequence 2, Application US/09978729A

Patent No. US20020178465A1

GENERAL INFORMATION:
APPLICANT: Yanofeky, Martin F.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
ITLE OF INVENTION: Selective Control of Lignin Biosynthes:
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/09/978,729A

CURRENT FILING DATE: 2002-06-10

PRIOR APPLICATION NUMBER: US 60/090,649
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Best Local Similarity:
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Publication No. US20020194645A1
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Alignment Scores: Pred. No.:
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PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 2
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PRIOR FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 242
                                                                                                                                                                                                                                              FILE REFERENCE: 19452A-000940US
CURRENT APPLICATION NUMBER: US/09/981,087A
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                APPLICANT: Liljegren, Sarah
APPLICANT: Farrandiz, Cristina
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Selective Control of Lignin Biosynthesis in
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/090,649 PRIOR FILING DATE: 1998-06-25
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APPLICANT: Vanofsky, Martin F.

APPLICANT: Pelaz, Soraya

APPLICANT: Ditta, Gary

APPLICANT: Ditta, Gary

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants

TITLE OF INVENTION: Exhibiting Modulated Reproductive Development

FILE REFERENCE: 19452A-002400US

CURRENT APPLICATION NUMBER: US/99/853,450

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 61

SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
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OTHER INFORMATION: APETALA1 (AP1)
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ditta, Gary
APPLICANT: Ditta, Gary
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants
TITLE OF INVENTION: Exhibiting Modulated Reproductive Development
FILE REFERENCE: 19452A-0024400US
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT APPLICATION NUMBER: US/09/853,450
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09853450 Publication No. US20020194645A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Yanofsky, Martin F. APPLICANT: Pelaz, Soraya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                    263 ATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACC
                                                                                                                                                                                                                                                                                                 LysileGluLeuLeuGluArg
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                                                                 ATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCG
                                                                                                                  TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT
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                               IleAlaProGluSerAspValAsnThrAsnTrpSerMetGluTyrAsnArgLeuLysAla
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Ditta, Gary
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-Q=/cgn2 1/USPTO_spool/US10020338/runat_24062003_102356_21591/app_query.fasta_1.775
-DB=Published_Applications_AA -QEMT=fastan -SUPFTX=rxpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALICN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10020338_@CGN 1 1 17 @runat 24062003 102356_21591
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOD=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Sequence 4, Appli
Sequence 2, Appli
Sequence 6, Appli
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399 38.7 242 9 US-09-981-087A-2 399 38.7 242 9 US-09-978-312A-2 399 38.7 242 10 US-09-978-740A-2 392 31.3 259 9 US-09-853-450-12 31.3 259 9 US-09-853-450-12 31.3 259 9 US-09-853-450-2 31.3 259 9 US-09-853-450-3 22.3 13.3 259 9 US-09-853-450-3 23.4 9 US-09-853-450-3 24.5 26.7 248 9 US-09-978-730A-4 25.6 2 246 9 US-09-978-730A-4 25.6 2 246 9 US-09-978-730A-6 25.7 25.0 240 9 US-09-978-730-12 25.6 2.9 25.6 9 US-09-978-730-12 25.6 2.9 25.6 9 US-09-819-142-13 25.7 25.0 173 9 US-09-819-142-13 25.8 22.9 25.6 9 US-09-819-142-13 25.9 25.0 173 9 US-09-819-142-13 25.9 25.0 173 9 US-09-819-142-13 25.0 22.1 25.0 10 US-09-978-73-130 25.1 22.1 23.8 9 US-10-286-264-26 25.3 22.9 25.6 9 US-10-286-264-26 25.4 22.7 507 10 US-09-819-142-14 25.5 22.1 23.8 9 US-10-286-264-26 25.5 22.1 23.8 9 US-10-286-264-26 25.5 22.1 23.9 10 US-09-819-142-14 25.5 22.1 23.8 9 US-09-819-142-14 25
8.7 242 9 US-09-981-087A-2 8.7 242 9 US-09-978-3182A-2 8.7 242 10 US-09-978-740A-2 8.7 242 10 US-09-978-740A-2 8.7 242 10 US-09-978-740A-2 8.1 255 9 US-09-853-450-14 7.1 251 9 US-09-853-450-12 7.1 251 9 US-09-853-450-20 1.3 250 9 US-09-853-450-30 0.5 234 9 US-09-853-450-30 0.5 234 9 US-09-853-450-30 0.5 234 9 US-09-853-450-30 0.5 234 9 US-09-978-730-4 6.7 248 9 US-09-978-732A-4 6.7 248 9 US-09-978-732A-4 6.7 248 9 US-09-978-730-4 6.7 248 9 US-09-978-730-4 6.6 246 9 US-09-978-730-4 6.2 246 9 US-09-978-740-7 6.2 246 9 US-09-978-740-7 6.2 246 9 US-09-978-740-7 6.2 246 9 US-09-819-142-14 7.1 248 9 US
42 9 US-09-981-087A-2 42 9 US-09-978-730-2 42 10 US-09-978-730-2 42 10 US-09-978-730-2 42 10 US-09-978-730-2 42 10 US-09-853-450-10 50 9 US-09-853-450-12 50 9 US-09-853-450-28 50 9 US-09-853-450-30 37 9 US-09-853-450-30 37 9 US-09-853-450-30 38 9 US-09-9853-450-30 39 9 US-09-9853-450-30 40 9 US-09-978-730-44 48 9 US-09-978-730-44 49 9 US-09-978-730-44 49 9 US-09-978-730-46 46 9 US-09-978-730-46 46 9 US-09-978-730-66 46 9 US-09-978-730-66 46 10 US-09-978-730-62 40 9 US-10-295-403-70 40 9 US-10-295-403-68 41 0 US-09-978-728B-1 42 10 US-09-819-142-14 43 10 US-09-876-187-6 44 10 US-09-876-187-6 45 10 US-09-876-187-6 46 10 US-09-876-187-6 47 10 US-09-876-187-6 48 10 US-09-876-187-6 49 US-09-876-187-6 49 US-09-876-187-6 40 US-09-876-187-6 40 US-09-876-187-6 40 US-09-876-187-6 40 US-09-876-187-8
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978-382A-2 978-740A-2 978-740A-2 978-740A-2 978-740A-2 978-7450-10 853-450-12 853-450-30 853-450-30 853-450-30 853-450-30 853-450-30 853-450-30 853-450-30 853-450-30 853-450-30 853-450-30 978-730A-4 978-740A-4 978-740A-6

RESULT 1 US-09-853-450-8 US-09-853-450-8 Sequence 8, Application US/09853450 Publication No. US20020.94645A1 GENERAL INFORMATION: APPLICANT: Panofsky, Martin F. APPLICANT: Pelaz, Soraya APPLICANT: Ditta, Gary APPLICANT: The Regents of the University of California TITLE OF INVENTION: Combinations of Genes for Producing Seed Plants TITLE OF INVENTION: Exhibiting Modulated Reproductive Development FILE REFERENCE: 19452A-002400US CURRENT APPLICATION NUMBER: US/09/853,450 CURRENT APPLICATION NUMBER: US/09/853,450 CURRENT FILING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 61 SEQ ID NO 8 LENGTH: 273 TYPE: PAT CORGANISM: Zea mays FEATURE: OTHER INFORMATION: APETALA1 (AP1) US-09-853-450-8 Alignment Scores: Alignment Scores: 3.31e-46 Matches: 109 Percent Similarity: 99.09% Conservative: 0

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Best Local Similarity:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
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ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-UD 2143
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,227
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Maize and Cauliflower APETALA1 Gene
TITLE OF INVENTION: Products and Nucleic Acid Molecules Encoding Same
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TOPOLOGY: lines-
LECHTE
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Search completed: June 24, 2003, 14:13:23 Job time: 17.5 secs

ADDRESSEE: Fish & Richardson P.C. STREET: 4225 Executive Square, Su

Square, Suite 1400

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Query Match:
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               Sequence 2, Application US/08659188 Patent No. 6002069
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/360
FILING DATE: 12-21-94
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
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REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
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 APPLICANT:
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TYPE: amino acid
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Best Local Similarity:
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Sequence 2, Application US/08655227 Patent No. 6025483 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MEDIUM TYPE: Floppy
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ADDRESSEE: Campbell and Flores
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Matches:
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                                                                                                                                                                         Sequence 4, Application US/09398326 Patent No. 6355863
                                                                                                GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Seed Plants Exhibiting In
TITLE OF INVENTION: Reproductive Development
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APPLICATION NUMBER: US 08/592,2:

RILING DATE: 26-JAN-1996

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UD 3:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 4:
                                                                   NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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OPERATING SYSTEM:
                   CITY:
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                              E: Campbell and Flores LLP
4370 La Jolla Village Drive,
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Best Local Similarity:
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                                                                            Sequence 2, Application Patent No. 5844119
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
              APPLICANT: Weigel, Detlef
TITLE OF INVENTION: Genet
TITLE OF INVENTION: Flower
NUMBER OF SEQUENCES: 2
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: Patentin Release #1.0,
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                                                                                                                   Application US/08576156
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                          Genetically Modified Plants Having Flower Development
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Patent No. 6025543
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                    STREET: 43..
CITY: San Diego
CTATE: California
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                        APPLICANT: Yanofsky, Martin F.
APPLICANT: Weigel, Detlef
TITLE OF INVENTION: Seed Plants Exhibiting Early Reproductive
TITLE OF INVENTION: Development and Methods of Making Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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TOPOLOGY: linear
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4370 La Jolla Village Drive,
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Matches:
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Query Match:
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Patent No. 6127123
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                                                                                                                                    APPLICANT: Yanofsky, Martin F.
TITLE OF INVENTION: Gauliflower Floral Meristem Identity
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 80
ATTORNEY/AGENT INFORMATION:
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LENGTH: 253 amino acids
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                     COUNTRY: UZIP: 92122
                                                                                                                          ADDRESSEE:
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                                                                    San Diego
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                                                                                                      E: Campbell & Flores LLP
4370 La Jolla Village Drive,
                                                  United States
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   TITLE OF INVENTION: Seed Plants E
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                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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TYPE: amino acid
TOPOLOGY: linear
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CLASSIFICATION:
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                                                                                                                                                                    E: Campbell and Flores
4370 La Jolla Village Drive,
                                                                                                                     USA
                                                                                                                                                                                                                                               Yanofsky, Martin F.
VENTION: Seed Plants Exhibiting Inducible Early
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RESULT 9
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Query Match:
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Patent No.
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME: Cambbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-1
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                                                                                                                    COUNTRY: USA
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4370 La Jolla Village
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Matches:
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Best Local Similarity:
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TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acids
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Atent No. 6355863
                                                                                                                                                                                                          STREET: SAN Diego CITY: San Diego CTATE: California
CLASSIFICATION: PRIOR APPLICATION NUMBER: '
                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores LLP
STREET: 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yanofsky TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                       APPLICATION NUMBER:
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ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 37
TELECOMMUNICATION INFORMATION:
TOT.EPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08592214A Patent No. 5811536
GENERAL INFORMATION:
APPLICANT: Yanofsky, Martin F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (619) 535-90
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acid
TYPE: amino acid
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                          APPLICANT: Yanofeky, Martin F.
TITLE OF INVENTION: Cauliflower Floral Meristem Identify
TITLE OF INVENTION: Genes and Methods of Using Same
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                           CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
     APPLICATION NUMBER:
                                                                                                                                            COUNTRY:
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Best Local Similarity:
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; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-655-227-8
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SOFTWARE: PATENTIN Release #1.0, Ve. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,241
FILING DATE: 05-JUN-1996
CLASSIFICATION: CLASS 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1894
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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Weigel, Detlef
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US-09-149-976-8
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yanofsky, TITLE OF INVENTION: CTITLE OF INVENTION: CNUMBER OF SEQUENCES:
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                          APPLICATION NUMBER: US/0:
FILING DATE: 09-SEP-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                APPLICATION NUMBER: US 0: FILING DATE: 26-JAN-1996 ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn J
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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CITY: San Diego
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4370 La Jolla Village Dr
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Cathryn A.
BER: 31,815
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Cauliflower Floral
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6002069
GENERAL INFORMATION:
                                            APPLICATION NUMBER: US/08/659,188
FILING DATE: 05-UUN-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UD 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yanofsky
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 2
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4370 La Jolla Village Drive, Suite 700
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Reproductive Development and Methods of
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Query Match:
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; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-659-188-8
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US-08-655-227-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Yanofs
TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                   REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,81
                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Pr.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                            FILING DATE: 05-JUN-1996
CLASSIFICATION: 800
                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 05-JU
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CITY: San Diego
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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USFTO_spool/US10020338/runat 24062003 102355 21531/app_query.fasta_1.775
-Q=/cgn2 1/USFTO_spool/US10020338/runat_24062003 102355 21531/app_query.fasta_1.775
-DB=Issued_patents_AA-CpMT-fastan -SUPFIX=rai -MINMARCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10020338 @CGN 1 1 28 @runat 24062003 102355 21531 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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    protein search, using frame_plus_n2p model

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Ygapop 10.0
Fgapop 6.0
Delop 6.0
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2: /cgn2_6/ptcdatta/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdatta/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptcdatta/1/iaa/6B_COMB.pep:*
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US-08-655-227-4
US-08-655-227-4
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9-149-976-1	-08-655-227	-08-659-188-1	-08-592-214A-	-09-398-326-1	S-09-149-976-	S-08-655-241-1	-08-655-227-1	59-188-	92-214A	9-398-326-1	-09-149-976-1	-08-655-241-1	US-08-655-227-10	59-188-1	4A-	-349-677-	-09-105-652-	S-09-067-	-09-398-326-	-09-149-976-	-08-655-241-	-08-655-227-	-08-659-188-	-08-592-214A	-09-149-976-	-08-592-214A	9-398-326-	-08-655-241-	-08-655-227-	-08-659-188-	8-576-156-
equence 12, App	nce 12, Ap	equence 12, App	equence 12, Ap	equence 14, Ap	equence 14, App	equence 10, App	equence 10, App	equence 10, App	equence 10, Ap	equence 10, App	equence 10, App	equence 2, Appl	equence 2, Appl	equence 2, Appl	equence 6, Appl	equencé 6, Appl	equence 2, Appl														

ALIGNMENTS

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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,214A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 3,815
REFERENCE/DOCKET NUMBER: P-UD 1927
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION S35-9001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Yanofs
                                                TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS:
LENGTH: 273 amino acid
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CITY: San Diego
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This sequence is the Brassica oleracea AP1 protein. This sequence was used to isolate DNA encoding the Arabidopsis thaliana CAULIFICOMER (CAL) protein of the invention. An expression vector containing the CAL DNA sequence can be used to convert shoot meristems to floral meristems,
                                                     Disclosure; Fig 2; 93pp; English
                                                                         Cloned CAULIFLOWER genes - and vectors meristems to floral meristems
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tion; angiosperm; AP1 gene.
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                         AAGATTGAGACCATACAAAAA 583
                                                                                               ATGGGTCGCGGCAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACC
LysileGluLeuLeuGluArg 107
                                                   IleAlaProGluSerAspSerAsnThrAsnTrpSerMetGluTyrAsnArgLeuLysAla
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AlaAlaGluMetGlyArgGlyProValGlnLeuArgArgIleGluAsnLysIleAsnArg
           AATCAGGATATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAAACAAGATAAATCGG 31:
                                                    CCACCCCGGCCG-----CCGTGCGCGCCATAGACACAAGAGCCGACAGCTAGATCGCGA
                                                                      LeuGluArgHisLeuIlePhePro---
                                                                                                        AsnArgProLeuProSerSerSerProSerSerLeuAlaCysAlaProLeuGluSerArg
                                  ProThrArgProHisHisHisCysCysAspGluSerGluArgGluArgValGlyGlyGlu
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                           results in replacement of a few basal flowers by inflorescence shoots that are not subtended by flowers. When API is ecotopically expressed in shoot meristem, the shoot meristem is converted to floral meristem and early flowering can occur. The invention relates to floral meristem identity genes API, LFY and especially CAL (see AAP76885-97 and AAP99437) and their gene products (see AAW23811-18), and their use in converting shoot meristem to floral meristem and in promoting early flowering in transgenic plants, especially angiosperms such as cereal plants, leguminous plants, oilseed plants, trees, fruit-bearing plants or ornamental flowers.
                                                                                                                                                                                                                                                                                           Cauliflower floral meristem identity genes and related used to develop products for converting shoot meristem meristem and promoting early flowering in an anglosperm
                                                                                                                                                                                 This sequence comprises the Brassica oleracea APETALA (AP1) gene product that is involved in the conversion of shoot meristem to floral meristem. B. oleracea AP1 cDNA and genomic DNA sequences are provided (see AAT76886 and AAT76893). Mutation of the AP1 gene
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N-PSDB; AAT76886 and AAT76893
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99US-0161350

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RESULT 13
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(first entry)

AAG34120

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                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                             Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a maize MAD3 protein, designated ZmMADS3. The ZmMAD3 protein is essential for flower development and is active in flowers, in particular, in immature flowers and female flowers, but also in the mature embryo sac of maize. The ZmMAD3 protein is also active in nodes and adjacent cell layers. ZmMAD3 polynucleotides and polypeptides are useful influencing flower structure, function and seed or fruit development in transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide encoding ZmMADS3 protein, for use in cloning and expression in plant a nucleic acid sequence encoding protein influencing flower structure, function and/or its seed and/or fruit development
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N-PSDB; AAF85192.
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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LysIleGluThrIleGlnArgCysHisLys
                     AAGATTGAGACCATACAAAAATGTCACAAG
                                           TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT
                                                                                                                                                                                       PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGluIleSerValLeuCysAsp
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Best Local Similarity:
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The present sequence is the rice MADS box protein. The MADS box gene be used for regulating plant branching to provide ornamental or agricultural plants. In addition, plants with value-added properties an increased yield can be produced using the MADS box gene.
                                                                                                                                                            Rice MADS box gene for or agricultural plants
                                                                                                                                                                                                                                                                                                                            (TSUB )
(KOJI/)
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                                                                                                   2; Page 19; 43pp; Japanese
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KOJIMA
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                                                       25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

16-APR-1999

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99US-0126264.

99US-0126765.

99US-0127622.

99US-012762.

99US-0128234.

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99US-0130077.

99US-013045.

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US-10-020-338-8 (1-593) x AAY67553
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                                                                                                                          The invention relates to a new non-naturally occurring seed plant that comprises a first ectopically expressible nucleic acid molecule encoding a floral meristem identity gene product, provided that the seed plant does not contain a mutation in an endogenous TERMINAL FLOWER (TFL) gene that results in ectopic expression of CAL. The non-naturally occurring seed plant exhibits early reproductive development. The method of promoting early reproductive development can make breeding of long generation seed plants such as trees practical. The method can be used to increase floral meristem identity gene product expression in different crop fields at different times, resulting in a staggered time of harvest for the different fields. The present sequence represents a Zea mays
                                                                                                                                                                                                                                                               New transgenic seed plant exhibiting early reproductive develo comprises a CAULIFLOWER encoding nucleic acid and a non-mutant endogenous TERMINAL FLOWER gene -
                                                                                                                                                                                                                                                                                                        WPI; 2000-181843/16.
N-PSDB; AAZ57057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seed plant; floral meristem; mutation; TFL gene; CAL; reproduction; plant breeding; APl protein.
                                                                                                Sequence
                                                                                                                                                                                                                                               Claim 15;
                                                                                                                                                                                                                                                                                                                                     Yanofsky
                                                                                                                                                                                                                                                                                                                                                                          05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                             05-JUN-1996;
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263 ATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACC 322

Alignment Scores

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This sequence represents the APETALAL (API) amino acid sequence from corn. API is a floral meristem identity product, that promotes conversion of shoot meristem to floral meristem in an angiosperm. Vectors containing the API gene can be used to create transgenic plants. API nucleotide sequences can be used to promote early reproductive development in seed plants which is useful for accelerating selective breeding programmes that require several rounds of crossing to produce plants with disease
                                                                                                                                                                                                                                                                                                                                                              Purified nucleic acids encoding APETALA 1 (AP1) reproductive development in seed plants, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Corn APETALA1
                     and insect resistance. The nucleotide for promoting early reproductive devel
                                                                                                                                                                                                                                                                                     Claim 1; Column 63-64; 50pp; English.
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N-PSDB; AAZ92144.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APETALA1; AP1; floral meristem identity; early reproductive development; transgenic plant; selective breeding programme; disease resistance; corn
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as trees.
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                   are particularly useful long generation seed
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                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This protein comprises maize floral meristem identity gene product (ZAP1, the orthologue of the Arabidopsis APETALA (AP1) gene product (see AAM393131) that is involved in the conversion of shoot meristem to floral meristem. Mutation of the AP1 gene results in replacement of basal flowers by inflorescence shoots that are not subtended by flowers. The invention relates to an expression vector comprising a nucleic acid sequence encoding a floral meristem gene product operably linked to a heterologous regulatory element (see AAV02770-75). The floral meristem gene product is selected from AP1, LFY (LEAFY) and CAL (CAULIFLOWER) (see AAW39131-38). The expression vector is used to convert shoot meristem tissue to floral meristem tissue in transgenic plants, especially angiosperms or gymnosperms, thereby promoting early reproductive development in these plants.
                                                                                                                                                                                                                                                                                                                                                                                        est Local Similarity:
ery Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding API floral meristem identity gene product from cauliflower and maize - useful for promoting early reproductive development and controlling the time of seed-derived crop harvest in e.g. grapes, beans, corn, wheat, etc
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                                                                                          SerArgMetAspLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluLysAlaLeu
                                                                                                            TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT
                                                                                                                                                        AlaGluValAlaValIleValPheSerProLysGlyLysLeuTyrGluTyrAlaThrAsp
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                           ileSerAlaGluSerGluSerGluGlyAsnTrpCysHisGluTyrArgLysLeuLysAla
                                                   ATTTCAGCTGAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCG
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                                                                                                                                                                                                                                                                                                                  The present sequence represents an APETALA1 (AP1) polypeptide. The All polypeptide is an ectopically expressible floral meristem identity gene product. The specification also describes CALIFIOWER (CAL) and LEAFY (LFY) gene products. CAL is involved in the conversion of shoot meristem to floral meristem. CAL is highly conserved among different angiosperms. The CAL polynucleotides may be used to shoot meristem to
                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                      detecting a polymorphism associated with caulifle modified cauliflower allele that does not encode
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LFY; flora
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                                                                                                                                                                                                                                                                                                         floral meristem, and to promote early flowering in angiosperms
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 TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTT
                                                                    PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGluIleSerValLeuCysAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence of a APETALA1 (AP1)
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                         Yanofsky MF
                                                                           05-JUN-1996;
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                                                                                                                              11-DEC-1997
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                                                                                                                                                                                                        transgenic
                                                                                                                                                                                                                      Floral meristem
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                                                                                                                                                                                                        plant; angiosperm;
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                                                 CALIFORNIA.
                                                                                                                                                                                                                                                                         (first
                                                                           96US-0659188
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                                                                                                                                                                                                                    identity gene;
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561.00
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99.09%
54.47%
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                                                                                                                                                                                                                      APETALA1; AP1; ZAP1;
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SXCCCCCCCCCCCCXPXTHHHXX This protein comprises maize floral meristem identity gene product ZAPI, the orthologue of the Arabidopsis APETALA (API) gene product (see AAM43326) that is involved in the conversion of shoot meristem to floral meristem. Mutation of the API gene results in replacement of basal flowers by inflorescence shoots that are not subtended by flowers. The invention relates to a recombinant nucleic acid that Use of floral meristem identity genes to convert shoot meristem t floral meristem - for promoting early reproductive development in the plants and control timing of seed-derived crop harvest(s) in e.g. grapes, beans, corn and wheat This protein comprises maize floral meristem identity Claim 6; Page 110-112; 147pp; English. N-PSDB; AAV06021 ä

Sequence 273 A.

comprises an inducible regulatory element (see AAV06025-28) operably linked to a nucleic acid molecule (see AAV06018-24) encoding a floral meristem identity gene product (see AAV4326-32), especially API, CAULIFLOWER (CAL) or LEAFY (LFY). The nucleic acids are used to

transgenic plants, thereby promoting early reproductive in these plants. This can be useful for manipulating the

ve development the time of time

convert shoot meristem tissue into floral meristem tissue

crop harvest in seed-derived crops and to hasten breeding

RESULT 6
AAW39134
ID AAW3
XX AAW3
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AC AAW3
XX O8-J
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XX Flor
XX tran 밁 Ş 밁 Ş S 밁 S 밁 밁 S 문 8 US-10-020-338-8 (1-593) x AAW43329 Query Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Match: 563 503 443 383 323 101 263 81 61 41 21 ᆫ AAGATTGAGACCATACAAAAATGTCACAAG SerArgMetAspLysIleLeuGluArgTyrGluArgTyrSerTyrAlaGluLysAlaLeu GCGGAGGTCGCCGTCATCGTCTTCTCCCCCAAAGGCAAGCTCTATGAGTACGCCACCGAC MetGlyArgGlyLysValGlnLeuLysArgIleGluAsnLysIleAsnArgGlnValThr ATGGGTCGCGGCAAGGTGCAGCTGAAGCGGATAGAGAACAAGATAAATCGGCAGGTGACC LysIleGluThrIleGlnLysCysHisLys ileSerAlaGluSerGluSerGluGlyAsnTrpCysHisGluTyrArgLysLeuLysAla ATTTCAGCTGAAATCTGAAAGTGAGGGAAATTGGTGCCACGAATACAGGAAACTTAAGGCG AlaGluValAlaValIleValPheSerProLysGlyLysLeuTyrGluTyrAlaThrAsp PheSerLysArgArgAsnGlyLeuLeuLysLysAlaHisGluIleSerValLeuCysAsp TCCAGCATGGACAAAATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAAGGCTCTT TTCTCCAAGCGCCGCAACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGAC 561.00 99.09% 99.09% 54.47% 1.23e-50 (1-273) Length: Matches: Mismatches: Indels: Conservative: 592 110 273 109 0 1 0 100 562 80 502 60 442 40 382 20 322

Floral meristem identity gene product; APETALA1; AP1; transgenic plant; angiosperm; seed development; maize.

Maize floral meristem

identity gene product APETALA1

08-JUN-1998 AAW39134;

(first entry)

AAW39134

standard;

Protein;

273

AA

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RESULT 3
AAW69328
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                                                                                          SXCCCCCXXXXPAXXX
                                                                                                                                                                                                                                                                                          Alignment
Pred. No.:
  Query Match:
DB:
                       Percent Similarity:
Best Local Similari
                                                                                                            This sequence is the Zea mays AP1 protein (ZAP1). This sequence was used to isolate DNA encoding the Arabidopsis thaliana CAULIFLOWER (CAL) protein of the invention. An expression vector containing the CAL DNA sequence can be used to convert shoot meristems to floral meristems, especially to promote early flowering in angiosperms.
                                                                                                                                                                                                       Cloned CAULIFLOWER genes - and vectors meristems to floral meristems % \left( \mathbf{r}\right) =\left( \mathbf{r}\right) 
                                                                                                                                                                                                                                                      WPI;
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                                                                                          Sequence
                                                                                                                                                                                    Example
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DB; AAV58307.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                   Fig
                                                                                          273
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                       e; CAL gene; shoot meristem conversion; floral meristem;
promotion; angiosperm; AP1 gene; ZAP1.
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The present sequence represents a floral meristem identity gene product, APETALA1 (API), from Zea mays. The invention relates to a non-naturally occurring seed plant comprising a first ectopically expressible nucleic acid encoding a first floral meristem identity gene product, provided that the first nucleic acid is not ectopically expressed due to a mutation in an endogenous TERMINAL FLOWER gene.
                                                                                                                                      Transgenic plant comprising an ectopically expressed floral meristem gene - for promoting early reproductive development and controlling the time of seed-derived crop harvest(s) in e.g. grapes, beans, corn, wheat, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW43112 standard;
                                                                                                                                                                                                                                                                                                                                 11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                         WO9746077-A1
                                                                                                                                                                                                                                                                                                                                                                                                      angiosperm
                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic plant; AP1; CAULIFLOWER;
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                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                  05-JUN-1996;
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                                                                                                                                                                                                                                   Yanofsky
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CAL; LEAFY;
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The invention describes a method of converting shoot meristem to meristem, especially in order to promote early reproductive develon an angiosperm, which comprises introducing a first ectopically

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                                                              ATTCTTGAACGTTATGAGCGCTACTCTTATGCTGAAAAGGCTCTTATTTCAGCTGAATCT 517
                                                                                                                                                                                                                     AACGGGCTCCTGAAGAAGGCGCACGAGATCTCCGTCCTCTGTGACGCCGAGGTCGCCGTC
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                                                                                                                                                                                                                                                                                                                                                gene product that is involved in the conversion of shoot meristem to floral meristem. The sequence was deduced from an isolated cDNA clone (see AAT99437). ZAP-1 is the maize orthologue of Arabidopsis APETALA (AP1) (see AAW23811). Mutation of an AP1 gene results in replacement of a few basal flowers by inflorescence shoots that are not subtended by flowers. When AP1 is ecotopically expressed in shoot meristem, the shoot meristem is converted to floral meristem and early flowering can occur. The invention relates to floral meristem identity genes AP1, LFY and especially CAL (see AAT76885-97 and AAT99437) and gene products (see AAW23811-18) and their use in converting shoot meristem to floral meristem and in promoting early flowering in transgenic plants, especially angiosperms such as cereal plants. Leguminous plants, of the convertion and the convertion of the conv
                                                                                                                                                                                                                                                                                          Sequence
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SUMMARIES

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Minimum
Maximum
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-Q=/cgn2_1/USPTO_spool/US10020338/runat_24062003_102353_21487/app_query.fasta_1.775
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Maximum Match 100%
Listing first 45 s
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1: /SIDSZ/gcgdata/
2: /SIDSZ/gcgdata/
3: /SIDSZ/gcgdata/
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             908470 seqs, 133250620 residues
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution. printed,

Result 15 16 17 18 19 20 20 21 23 435.54 426.55 420.66 42 Score Match Length DB IJ AAY67550 AAY78880 AAB19241 AAW69327 AAW23813 AAB19242 AAY67551 AAY78881 AAW23811 AAW23811 AAW3109 AAW39131 AAW43326 AAG17300 AAW69329 AAW43110 AAW39132 AAW43327 AAB19243 AAY67552 AAY78882 AAW69330 AAW43111 AAR99636 AAY69920 AAW43328 AAW39133 AAY78883 AAB73250 AAB19244 AAY67553 AAW23812 AAY84912 AAG34120 AAB68357 AAG33291 AAW43329 AAG33290 Amino acid sequenc B. oleracea AP1 pr Brassica oleracea Arabidopsis floral Arabidopsis LEAFY APETALA1 gene prod Arabidopsis floral Arabidopsis floral Arabidopsis thalia Arabidopsis thalia APETALA1 gene prod Cauliflower floral Cauliflower floral Amino acid sequenc A. thaliana AP1 pr APETALA1 (AP1) nuc Description Eucalyptus SQE-2L MADS box protein. Amino acid sequenc B. oleracea var. b Cauliflower APETAL Brassica oleracea Amino acid sequenc Arabidopsis thalia Cauliflower floral APETALA1 gene prod Brassica floral me Brassica floral me Brassica oleracea APETALA1 gene pro Amino acid sequeno Zea mays protein 1 Brassica oleracea Rice MADS box prot Zea mays protein i Amino acid sequenc Petunia MADS box Maize floral meri Zea mays AP1 prote APETALA1 gene prod Arabidopsis floral Corn APETALA1 Amino acid sequenc Zea mays ZAP1 Zea mays protein

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SULT 1
NG33290 AAG33290 standard; Protein; 164 AA.
AAG33290;
18-OCT-2000 (first entry)
Zea mays protein fragment SEQ ID NO: 40313.
Protein identification; signal transduction pathway; metabolic

hybridisation assay; genetic mapping; gene expression control; promoter termination sequence; corn. promoter;

Zea mays subsp. mays.